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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-NN1155-
271000-628-a09&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 175.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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BF945949
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                                                                                                  TGAGCGAGATGACCAGCTCCGGC 152
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TGAGAGAAATGACCACGTCGGGC
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                                                                                                                                   Conservative
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/note="Organ: nervous normal; Vector: puc18; Site 1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                      tissue mRNA and cDNA amplification were performed
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 175)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
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                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                  /note="Organ: nervous normal; Vector: pucl8; Site 1: SmaI; Site 2: SmaI; A mini-Tibrary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
/clone_lib="NN1155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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65.1%;
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                                                                                                                                                                                       Score 36.6;
Pred. No. 32;
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RESULT 3 BF408161

DEFINITION

BF408161 186 bp mRNA UI-R-BJ2-bra-d-05-0-UI.s1 UI-R-BJ2 Rattus

norvegicus

linear

EST 28-NOV-2000

cDNA clone

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SOURCE
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BF408161.1
                                     BF408161 186 bp mRNA UI-R-BJ2-bra-d-05-0-UI.sl UI-R-BJ2 Rattus UI-R-BJ2-bra-d-05-0-UI 3', mRNA sequence.
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POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coordinated Laboratory
University of Iowa
375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 186)
Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Seq_primer: M13 Forward
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319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-R-BJ2-bra-d-05-0-UI"
//lab host="DH10B (Life Technologies)"
/clone lib="UI-R-BJ2"
/clone lib="UI-R-BJ2"
/clone lib="UI-R-BJ2"
/clone lib="UI-R-BJ2"
/clone lib="UI-R-BJ2"
/clone lib-"Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, atrium at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soarse, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Pred. No. 3.2e+02;
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Rattus norvegicus (Norway rat)
                                                                       AA429110
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgan.com) The following repetitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa 375 Newton Road ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coordinated Laboratory for Computational Genomics
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Bonaldo, M.F., Lenno
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                                             AA429110.1 GI:2110653
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Normalization and subtraction: two
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Seq_primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                      GGGGGGGGGGCTCCAGCCCACACTTAGTGCATCCGGAGCCCGAAGCCCAGCCTCCCGCTC 76
                                                                                                                                                                                                                                                                              CCCGGCTGCCCAGCGGCCACGGACTAGACACTCATCCCCCGGCCCATGCCAGGAGGCCG
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sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="UI-R-BJ2"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified /note="Vector: pT/T3D-Pac (Pharmacia) with a modified /note="Vector: pt/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 plibrary is a subTracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
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/db xref="taxon:10116"
/clone="UI-R-BJ2-bra-d-05-0-UI"
/lab host="DH108 (Life Technologies)"
/clone_lib="UI-R-BJ2"
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/mol_type="mRNA"
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54.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32.6; DB 2;
Pred. No. 3.2e+02;
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Matches
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 127)

1 (bases 1 to 127)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                           AA429110 127 bp mRNA linear EST 16-OCT-1 zv78c11.rl Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759764 5' sīmilar to TR:G307309 G307309 HISTONE H4. [1] ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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(bases 1 to 127)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marrin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997

Unpublished (1997)
                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AA429110
AA429110.1 GI:2110653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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Location/Qualifiers
                                                                                                                                                                                                                                                  sapiens (human)
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:759764"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 5.1e+02;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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M., Martin,J.,
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                                                                                                                                                                                      TITLE
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                   Unpublished (2004)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38
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CL176108.1
GSS.
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                                                                                                                                                                            Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W., Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J. A. GeneThresher methylation filtered genomic sequences from Sox.
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor (sorghum)
Sorghum bicolor
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-Merck EST Project 1997 Unpublished (1997) Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                              (bases 1 to 152)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares total_fetus_Nb2HF8_9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
polylinker; Site_1: Not Io; Site_1: Not Io; Site_2: Eco RI; 1st strand
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) prime;
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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                       St. Louis, MO 63108, USA
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Pred. No. 5.1e+02
0; Mismatches 3:
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Length 127;

0

Gaps

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sequences from Sorghum

GSS 06-JAN-2004 iltered library

genomic survey

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JOURNAL COMMENT
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ORGANISM
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CL176108/c
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                                                                                                                     mail: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seg primer: T3 Reverse
Class: shotonn
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Email: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seq primer: T3 Reverse
Class: shotgun
                                                                                                                                                                                                                                             Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                  Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W., Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. GeneThresher methylation filtered genomic sequences from Sor,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD-clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 152)
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Sorghum bicolor
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Location/Qualifiers
                                                                               quality sequence stop: 152.
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314 615 5975
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104)"
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
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/clone="10892902"
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Pred. No. 7.2e+02;
0; Mismatches 23
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Sozghum bicolor (sorghum)

Sozghum bicolor

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Clade; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 152)

Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,

Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,

Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.

GeneThresher methylation filtered genomic sequences from Sorghum
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                                                                                                                                                                                                                                                                                                                                                                                             Email: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seg_primer: SWfor Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004)
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Location/Qualifiers
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                      prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a
methylation-filtered library.
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104)"
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/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                 note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
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Pred. No. 7.2e+02;
0; Mismatches 23;
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Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, S
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Plate: 382 row: e column: 22
Seq primer: SWfor Forward
Class: shoton
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Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,
Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,
Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
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104_382_10892902_148_31762_118 Sorghum methylation-filtered library
(LibID: 104) Sorghum bicolor genomic clone 10892902, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                   clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                    clone="10892902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Sorghum bicolor"
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                                                                                                                                           Score 31.2; DB 9;
Pred. No. 7.2e+02;
0; Mismatches 23;
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Pred. No. 7.2e+02;
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1 (bases 1 to 135)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Homo sapiens
                                   RC0-TN0078-310700-031-f03
CV406622
CV406622.1 GI:52802125
EST.
                                                                                                         CV406622
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This sequence was derived from
Project. http://www.ludwig.org.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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CV406622
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/db_xref="taxon:9606"
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/dev_stage="Adult"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                 Department of Biological Sciences Stanford University
                                                Maize genomic sequences Unpublished (2001) Contact: Walbot V
                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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This sequence was derived from the
Project. http://www.ludwig.org.br.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Zea mays
Zea mays
Class: transposon-tagged.
Location/Qualifiers
                                       Email: walbot@stanford.edu
Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1006122 column: 15
                                                                                                                              Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                              Contact: Walbot
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Unpublished (2001)
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACCAG
                                                                                                                                                                                                                                                                                                                                  (bases 1 to 168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev trage="mdult"
/lab_host="DH10B"
/clone lib="1006 - RescueMu Grid G"
/clone lib="1006 - RescueMu Grid G"
/clone lib="1006 - RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmbb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mol type="genomic DNA"
cultivar="mixed background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:4577"
tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Zea mays"
                                                                                                                                                                                                                      of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:16822338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.9%;
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Pred. No. 1e+03;
0; Mismatches 34,
                                                                                                                                                                                                                                                                                        found using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 bp
RescueMu
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                                                                                                                                                                               94304,
                                                               by 2 different sequence from s
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                                                                                                                                                                                                                                                                                          engineered
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                                                                                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear GSS 08-NOV-2001
Zea mays genomic, genomic
                                                                                                                                                                               US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                          RescueMu
                                                                 endonucleases.
source sequence
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REFERENCE
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DEFINITION
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestly, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Scardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI966631 151 bp mRNA linear EST 12-MAR-2002 id57a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5666983 3' similar to TR:P94852 P94852
                                                                                                Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DN
Washington University Genome Sequencing Center I
obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
MGI:1953309 This sequence now available from the IMAGE consortium,
                                                                                                                                                                                                                     Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PII PROTEIN. ;, mRNA sequence.
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                                                                                  (brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGCCGACGCGGAGCGTGGAGCCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTCGTCGGCTCGACGCCGACGCCGGACGCGTCCCTGGCGGACGCGACGGCCGAC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGACTCGACGATGAGCGAGATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.9%;
nilarity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells were transformed and then screened on LB plates with ampicillin."
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30.6; I pred. No. 1e+0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
                                                                                                                                  Douglas Melton DNA sequencing by equencing Center For information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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AUTHORS
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ORGANISM
                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI966631/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
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Best Local Similarity
                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 GATGACCAGCTCCGGCCGCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                     l (bases 1 to 151)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI966631 151 bp mRNA linear EST 12-MAR-2002 id57a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MWS1 Mus musculus cDNA clone IMAGE:5666983 3' similar to TR:594852 p94852
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus cDNA clone IMAGE:5666983
PII PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for clone orders contact: info@image.llnl.gov
                                                                               Contact: Douglas Melton, Klaus H.
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI966631.1 GI:16341036
                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCGAGGAGGTCCGCGAGGCCCTCGCCGAGGTCGGCGTCACCGGCCTGACCGTCACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCAAGGGCTTCGGCCGCC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with smicrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; I
libraries representing EI0.5/12.5 pancreatic bud, E16.9
pancreas, newborn pancreas, adult pancreas, and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adulf, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "SWM-TN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lib="Melton Normalized Mixed Mouse Pancreas 1
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Pred. No. 2.8e+03;
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REFERENCE
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                                          Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                 5-PRIME,
CA002143
                                                                                                                                                                                                                                                                            CA002143 167 bp
HS06K10r HS Hordeum vulgare subsp.
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
MGI:1953309 This sequence now available from the IM
for clone orders contact: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
1 (bases 1 to 167)
Zhang, H., Potokina, E., Michalek, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                         CA002143.1 GI:24279125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGGCCGAAGCCCTTGACCTCGGTGACGGTCAGGCCGGTGACGCCGACCTCGGCGAGGG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             egcegecegageregrearerecteareregregageregecegecegecegaegaegarea 95
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five libraries representing EIO.5/12.5 pancreatic bud, EI6.5 pancreas, and adult pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                                                                                                                                                                                            mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Embryonic day 10.5, E12.5, adult, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Both for embryonic & newborn, male for adult and
adult islet"
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/strain="ICR"
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Pred. No. 2.8e+03;
0; Mismatches 32;
                                                                                                                                                                                                                                                                              vulgare
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  Weschke, W.,
                                                                            Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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  Stein, N. and
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 TCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGC 115
                                                                                                                                                                                                Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 167)
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Barley ESTs from germinating
Unpublished (2002)
Contact: Stein Nils
Corrensetr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
                                                         Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research
                                                                                               Barley ESTs from germinating Unpublished (2002) Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                          CA002143.1 GI:24279125
EST.
                                                                                                                                                                                                                                                                                                                                                                                   5-PRIME, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                           HS06K10r
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Fax: 039482-5595
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Institute of Plant Genetics and Crop Plant Research (IPK)
CorrensBir. 3, 06466, Gatersleben, Germany
                                                                                                                                                            Graner, A.
                                                                                                                                                                               Zhang, H., Potokina, E., Michalek, W., Weschke, W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="vulgare"
/db_xref="GABI:257345"
/db_xref="taxon:112509"
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/mol_type="mRNA"
/cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo + scutellum"
/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
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Pred. No. 2.8e+03;
0; Mismatches 42;
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                                                                                                                                                                                                                                              Poaceae;
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                                                                                                                                                                                                                                                                 Tracheophyta;
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Insert Length: 167 Std Error:
Plate: 6 row: K column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                     1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CM1-ET0191-051200-626-b02
BF882476
                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF882476
Email: asimpson@ludwig.org.br
This sequence was derived from t
Project. This entry can be seen
                                                                                                                                                                                                                                   Proc. Natl. A
                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                      Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCGGCGCCGCCGCCGCACCGGAGAGGCCGGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGA 99
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                                                                               +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="HS" // Clone lib="HS" // Clone lib="HS" // Clone lib="HS" // Note="Wector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
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(clone="H$06K10"
/tissue_type="embryo + scutellum"
/dev stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
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db_xref="GABI:257345"
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Pred. No. 2.8e+03;
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    FAPESP/LICR Human the following URL
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High quality sequence start: 24
High quality sequence stop: 180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Coldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                       This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Res
Rua Prof: Antonio Prudente 109,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
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High quality sequence start: 24 High quality sequence stop: 180
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                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                Email: asimpson@ludwig.org.br
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/dev_stage="Adult"
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/mol_type="mRNA"
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ne_lib="ET0191"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Waugh R, Marshall DP
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                           Email: est@scri.sari.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
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/clone_lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/note="Vector: pSPORTI; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORTI.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome
                                                                                                                                             /clone="EBro04_SQ001_B16"
/tissue_type="root"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                      /dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                     /sub_species="vulgare"
/db_xref="taxon:112509"
                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Optic"
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                                                                                                                                                                                                                                                                                                                                                                                   Invergowrie, Dundee, DI
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Carc Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
On Sep 26, 2001 this sequence version replaced gi:15780290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EBro04_SQ001_B16_R root, Hordeum vulgare subsp. v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGCCGGAGCTGGTCATCTCGTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Dynamics/Computational Biology Scottish Crop Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare subsp. vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI777398.2
                                                                                                                                                                                                                                                                                                                                                                       Email: est@scri.sari.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Waugh R, Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare subsp. vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGCGGCGGGTTTTCTTCTCGGCGGCGATAGAGGTCTGTGAGCTGGAGGTCTTGACC
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                                                                                                                                                                                                                                                                                                                                 primer: M13 reverse
                                                                                                                                                                                                                                                                                                                                                sequence has a Phred quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
               /clone lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/note="Vector: pSPORT1; Site 1: Sall I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Function)
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                                                                                                                                         /clone="EBro04_SQ001_B16"
/tissue_type="root"
/tissue_type="3_week"
                                                                                                                                                                                                   species="vulgare"/db_xref="taxon:112509"
                                                                                                                                                                                                                                       mol_type="mRNA"
cultivar="Optic"
                                                                                                                                                                                                                                                                           organism="Hordeum vulgare subsp.
                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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Pred. No. 2.8e+03;
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vulgare c
project."
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Matches Query Match Best Local

72; Conservative

18.7%;

0,

Score 28.8; DB 4; Pred. No. 2.8e+03; 0; Mismatches 72

Indels

0

Gaps

0

DB 4;

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ACCESSION
VERSION
                                                                            RESULT 24
CE208692/c
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AUTHORS
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tigr-gss-dog-17000372681097
genomic survey sequence.
CE208692
CE208692.1 GI:35364347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
Tel: 301-838-0200
                                                              CE208692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frase
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                      CGCGGGCAGCGTCGCCTCGCTTGGGACGGAGTGGAGCAGGAGCGGGACCCGGAGTCCTAG
                                                                                                                                          CAGCCGCCATGGCGAGTGAGTTCCCCAG 103
                                                                                                                                                                       CCGCCGACTCGACGATGAGCGAGATGACCAG 145
                                                                                                                                                                                                                                    CTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301-838-0208
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shotgun
                                                                                                                                                                                                                                                                                                                                               /clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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Pred. No. 3.2e+03;
0; Mismatches 39
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                                           bog
đq 6
                                            Library
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                                                             DNA
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                                         linear GSS 25-SEP-20 Canis familiaris genomic,
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                                                                                                                                                                                                                                                                                                 Length 179;
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Fraser,C.M. and
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                                                           GSS 25-SEP-2003
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GSS.
GSS.
Canis familiaris (dog)
Canis familiaris
Canis
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HS17D13r
                                                                                                                                      Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                     Email: stein@ipk-gatersleben.de
Insert Length: 190 Std Error:
Plate: 17 row: D column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                         Barley ESTs from germinating seeds Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-PRIME, mRNA sequence.
CA004311
CA004311.1 GI:24281293
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Contact: Kirkness BF
The Institute for Genomic Research
The Institute for Genomics,
Seq primer: M13rev
                                                                                                                    Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                              Zhang, H., Potokina, E., Michalek, W.,
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1 (bases 1 to 190)
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Fax: 301-838-0208
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/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
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|mol_type="genomic DNA"
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Pred. No. 3.2e.
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JOURNAL COMMENT
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CA004311/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                 Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                                                                                  Barley ESTs from germinating seeds 
Unpublished (2002)
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HS17D13r HS Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
                                                                                                                                                                                      Insert Length: 190 Std Erro: Plate: 17 row: D column: 13 Seq primer: M13rev.
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CA004311.1 GI:24281293
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang, H., Potokina, E., Michalek, W., Weschke, W.,
                                                                                                                                                                                                                                                   Email: stein@ipk-gatersleben.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pooideae;
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/dev stage="0-16 hours after imbibition"
/lab host="XL10-Gold"
/clone_lib="HS"
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/sub_species="vulgare"
/db_xref="GABI:259529"
/db_xref="taxon:112509"
/clone="HS17D13"
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/clone="HS17D13"
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/cultivar="barke"
                                                                                   /mol_type="mRNA"
/cultivar="barke"
                                                                                                                        organism="Hordeum vulgare subsp. vulgare"
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/db_xref="GABI:259529"
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cDNA clone HS17D13
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RESULT 27
CN423515
LOCUS
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 GAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCTCATCGT 66
                                                                        Similarity 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 147 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fi
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geron Corporation
230 Constitution Drive, Menlo Park,
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GCTGCGGCGGCGGTGTCTCGCGTTCGGCGGGATTTCTCTTCGCTCCGGCTCGACCTAGGT 95
                                Conservative
                                                                          Conservative
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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: KhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                    /clone_lib="GRN_PREHEP"
/note="oligo dT primed, full-length enriched cDNA library
from DMSO-treated hBS cell line H9 (p22) maintained in
feeder-free conditions"
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/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
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Pred. No. 4e+0
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sapiens cDNA 5', mRNA sequence.
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4e+03;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 196)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                     Homo sapiens
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                                                                                                      sapiens (human)
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650 473 7760
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Length: 147 Std Error:
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/note="01igo dT primed, full-length enriched cDNA library
from DMSO-treated hBS cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 4e+03;
0; Mismatches 38;
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 cDNA Library Preparation: M. Bento Soares, Ph.D.,
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164 CGCCGAACGCGAGACACCGCCGCCGCAGC 192
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                            AI564785
tn37c01.x1 NCI_CGAP_Brn25
 Tissue Procurement: David N. Louis,
                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                        (CGAP/BTGAP), Tumc
Unpublished (1998)
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome

Clone distribution: NCI-CGAP clone distribution

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

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Unpublished (1998)
Contact: Robert Strausberg, Ph.D
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Tissue Procurement: David N. Louis, M.D.,
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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IMAGE:2169792 3',
 Rosenfeld M.D.,
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                                     Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
    Location/Qualifiers
                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 196)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
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tm80d10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2164435 3',
                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 277 Std Error: 0.00
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lab_host="DH10B"
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/clone="IMAGE:2169792"
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Pred. No. 4e+03;
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RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                         DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.lll.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
                                                                                                                                                                                                                                                                                                                           Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                           Ph.D.
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/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia)
modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                             /tissue type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2164435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2164435"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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sapiens cDNA clone IMAGE:2164435 3',
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CL601509
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OB_Ba0070005 3', g
CL601509
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1 CGGCCGGAGCTGGTCATCTCGCTCGAGTCGGCGGCGGAGCTGGTCATCTCGCT
                                                                                                                                                                                                                                                                                                                                      FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Scd Error: 0.00
Plate: 0070 row: O column: 05
Seg primer: CAC TCA TTA GGC ACC CCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                          Seq primer: CAC
Class: BAC ends.
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Kudrna, D., Muller, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrhartoideae;
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ilarity 57.3%;
Conservative
                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                 /organism="Oryza brachyantha"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="texon: 4533"
/clone="0B_Ba0070005"
/tissue_type="leaves"
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                               /clone_lib="OB_Ba"
/note="Vector: pagibacl; Site_1: HindIII; Site_
                                                                                                                                                                     'dev_stage="mature"
'lab_host="DH10B"
                                                                    18.3%;
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Ba Oryza brachyantha genomic clone
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Pred. No. 4e+03;
0; Mismatches
                                                                  Score 28.2; DB 9;
Pred. No. 4e+03;
                                                      Mismatches
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28 G
                                                             94 GAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CL601509 197 bp DNA linear GSS
CB Ba0070005.r OB Ba Oryza brachyantha genomic clone
OB Ba0070005 3', genomic survey sequence.
CL601509
CL601509.1 GI:48578762
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Oryza brachyantha
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Seq primer: CAC TCA TTA GGC ACC
Class: BAC ends.
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00
Plate: 0070 row: 0 column: 05
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Forbes Building Room 303, Tucson,
Tel: 520 626 955
Fax: 520 621,1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. ε
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://genome.arizona.edu
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                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                            /organism="Oryza brachyantha"
/mol type="genonic DNA"
/db xref="taxon:4533"
/clome="OB_Ba0070005"
/tissue_type="leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                   clone_lib="OB__Ba"
note="Vector:_pAGIBAC1;
                                                                                                                                                                                                                                                                                                  dev_stage="mature"
lab_host="DH10B"
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                                                                                                                                                                                                        4e+03;
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                                                                                                                                                                                        58;
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REFERENCE
AUTHORS
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ACCESSION
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PUBMED
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                                                                                                                                                                                                                             145 GCTCCGGC 152
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                                                                                                                                                                                                                                                                                                                                                                 43;
BE760525 130 bp mRNA linear RC2-CT0652-211200-011-b01 CT0652 Homo sapiens cDNA, BF760525.1 GI:12108425
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1 (bases 1 to 130)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deOllveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was derived from the FAPESE/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2kt2=RC2-CT0652-211200-011-b01kt3=2000-12-21kt4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: puc 18 forward
High quality sequence star
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC2-CT0652-211200-011-b01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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                                                                                                                                                                                  CGTCGGGC
                                                                                                                                                                                                                                                                                                                  CTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCA 144
                                                                                                                                                                                                                                                                       CTGGGTGGTGAGGGAAAGGACCACGTTGGGCGGTATGCTGGGTGAGAGAAATGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence start: 23 quality sequence stop: 130. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type= "man: 9606"
/db_xref="taxon: 9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Adult"
/clone_lib="CT0652"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                 <u>o</u>
                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; Length 130 Pred. No. 4.5e+03; O; Mismatches 25; Indels
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CT0652 Homo sapiens cDNA,
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RESULT 37
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                                                                                  Zea mays
Zea mays
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CB251950.1
EST.
                                                                                                                                                                                                                                                                                      CB251950
3529_1_19_1_H10.y_1
labs_Zea mays cDNA,
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1 (bases 1 to 130)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Magai,M.A., da Silva,R., Briones,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., Brunstein,A., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC2&t2=RC2-CT0652-211200-011-b01&t3=2000-12-21&t4=1)
seq_primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCGACGTGGTCATTTCTCTCACCACCCAGCATACCGCCCAACGTGGTCCTTTCCCTCA
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/mol type="mRNA"
/mb xref="taxon:9606"
/db xref="taxon:9606"
/dev stage="Adult"
/clone lib="CT0652"
/note="Torgan: colon; Vector: puc18; Site_1: SmaI; Site_2: /mote="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: /mote="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: /mote="Corgan: colon; Vector: puc18; Site_1: SmaI; Site_2: /mote="Corgan: colon; Vector: puc18; Site_1: SmaI; Site_2: /mote="Corgan: colon; Vector State By Coloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529 1 19 1 row: H o
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                                                                                    Stanford University
855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
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                                                        Email: walbot@stanford.edu
Plate: 3529_1_19_1 row: H
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/lab_host="E. coli XLOLR"
/clone_lib="3529 - 2 mm e:
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cultivar="B73"
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Fax: 650 725 8221
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855 California Ave,
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Department of Biological Sciences
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Plate: 606065 row: A column:
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/dev stage="2 mm"
/lab_host="E. coli XLOLR"
/lab_e lib="3529 - 2 mm ear tissue from Schmidt and Hake
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/db_xref="taxon:4577"
                                                                                                             /note="Organ: immature ear; Vector: pBK-CMV; Site_1: ECORI; Site_2: XhoI; Mixed ear tissue cDNA library f Schmidt lab"
                                                                                                                                                                /db_xref="taxon:4577"
/tissue_type="mixed"
/tev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/lab_nost="XLOLR (Stratagene)"
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mol type="mRNA"

cultivar="Ohio43"
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Plate: 606065 row: A column:
Location/Qualifiers
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855 California Ave, Palo
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                          /note="Organ: immature ear; Vector: pBK-CMV; Site_1:
ECORI; Site_2: XhoI; Mixed ear tissue cDNA library from
Schmidt lab"
                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/tissue_type="mixed"
/tissue_type="mixed"
/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="xIoLR (Stratagene)"
/clone_lib="606 - Ear tissue cDNA library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Zea mays"

/mol_type="mRNA"

/cultivar="Ohio43"
                                                                                sequence.
                                                      GI:12046804
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125 CGCCATCCGGC 135
                                                             Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
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1 (bases 1 to 163)
                        Email: walbot@stanford.edu
Plate: 1000069 row: F co
                                                                                                                                                                      Unpublished (1999)
Contact: Walbot V
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Location/Qualifiers
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Tel: 650 723 2227
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Contact: Walbot V
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/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR'S CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets were
also selected."
Location/Qualifiers
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/db_xref="dbEST:945002F06.X3"
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84
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[ (bases 1 to 180)
                                                                                                                                                                                                                                                                                                                                                                                                                      Barley EST's
Unpublished (2002)
Contact: Schulman AH
Institute of Biotechnology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
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/mol_type="mRNA"
/db_xref="db857:945002F06.X3"
                                                                                                                                                                                                                                     /clone="S0000800047F11F1"
/tissue_type="Callus"
/clone_lib="S00008"
                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                     note="Callus K19"
                                                                                                                                                                                                                                                                                                                     organism="Hordeum vulgare"
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Pred. No. 5e+03;
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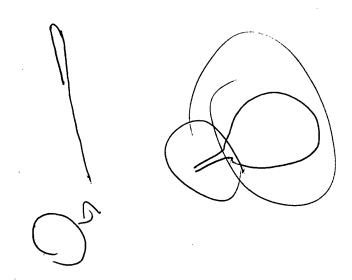
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AJ469411 S00008 Hordeum vulgare
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Contact: Schulman AH
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1 (bases 1 to 180)
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1924e03.bl WGS-ZmaysF (DH5a methyl
1924e03, genomic survey
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                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 184)
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                                         Lita Annenberg Hazen Genome Sequencing Center cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                   Zea mays
                                                                                            Unpublished (2002)
Contact: W. Richard McCombie
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               Tel: 516 367 8884 Fax: 516 367 8874
                                                                                                                        Genomic shotgun sequences from
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mccombie@cshl.org
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Class: shotgun
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APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINAT
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
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APPLICANT: Gordon-Kamm, William
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
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SOFTWARE: Microsoft Offic
SEQ ID NO 13
LENGTH: 154
          APPLICANT: Glassman,
APPLICANT: Gordon-K.
APPLICANT: Kinney,
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Gordon-Kamm, William Kinney, Anthony Lowe, Keith S.
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No. US20030036197A1
                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative (
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                                 Kimberly F.
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US-10-741-601-2931
US-10-741-601-3022
US-10-741-601-3115
US-10-741-601-3115
US-10-741-600-11671
US-10-741-600-11671
US-10-741-600-11762
US-10-741-600-11762
US-10-741-600-11855
US-10-741-600-1185
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Pred. No. 2.2e-37;
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2932, Ap
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3115, Ap
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11671, A
11762, A
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35083, A
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APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ANI
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER TYPE: OTHER
                                                                                                                                                                                                                                                                   CURRENT APPLICATION UNMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 154
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OTHER INFORMATION:
US-09-934-900-25
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Best Local Similarity
                                                                                                                       Matches 154;
                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT: Cahoon, Rebecca
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
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ORGANISM: Artificial Sequence
FEATURE:
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                   CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG
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Yadav, Naren
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Pred. No. 2.2e-37;
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US-09-934-900-25/c
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LENGTH: 154
TYPE: DNA
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Publication No.
                                                                                                                  SEQ ID NO 7
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Best Local Similarity
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                                                                                                                                                              TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES FILE REFERENCE: BB1535 US NA CURRENT APPLICATION NUMBER: US/10/734,947 CURRENT FILING DATE: 2003-12-11 PRIOR APPLICATION NUMBER: US 60/433,433 PRIOR PILING DATE: 2002-12-13 RIGHT PRIOR DATE: 2002-12-13 NUMBER OF SEQ ID NOS: 8
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SOFTWARE: Microsoft Office 97
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Booth, APPLICANT: Cahoc
                                                                                                                                             SOFTWARE: Microsoft Office 97
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FEATURE: OTHER INFORMATION: Artificial sequence containing a NotI site flanked by
                                                ORGANISM: Artificial Sequence
                                                                           TYPE: DNA
                                                                                               ENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
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Hitz, William D
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Yadav, Naren
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No. US20030054521A1
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, OTHER INFORMATION: 36-nucleotide repeats and having an EagI site at each end US-10-734-947-7
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Best Local S
Matches 154
                                                                                                                              Sequence 25, Application US/10981293 Publication No. US20050066390A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: McGonigle,
                                                                                                               GENERAL INFORMATION:
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SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10734947 Publication No. US20040128714A1
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APPLICANT:
TITLE OF IN
                                                                       APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rel
                                    APPLICANT:
                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 154
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                          61 CATCGTCGAGTCGGCCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
 INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
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                                                   Cahoon, Rebecca
Hitz, William D
                     Xinney, Anthony
Yadav, Naren
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Pred. No.
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                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS133
US-10-981-293-25
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OTHER INFORMATION:
US-10-981-293-25
                                                        Best Loc
Matches
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, App. Publication No.
                                                                                    Query Match
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PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/22696
PRIOR APPLICATION NUMBER: 60/22696
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: BB1476 US NA
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleotide Sequences
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                                                                                                                                                                                           LENGTH: 154
TYPE: DNA
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REFERENCE: BB1476 US NA
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Yadav, Naren
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Hitz, William D
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                                                        Score 154; DB 19;
Pred. No. 2.2e-37;
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Pred. No. 2.2e-37;
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APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AN FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
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US-09-887-194A-12/c
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                                                                                            CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                       GENERAL
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Best Local Similarity
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                                                                                                                                                                                                             APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
FILE REFERENCE: BB1449 US NA
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Glassman, Kimberly F. APPLICANT: Gordon-Kamm, William
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TYPE: DNA
ORGANISM: Artificial Sequence
                                  LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS106 and pKS124
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Lowe, Keith S.
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Pred. No. 6.3e-1
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PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 80
TYPE: DNA
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US-09-934-900-24/c
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                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
CURRENT FILING DATE: 2001-08-22
                                                                                                                                         APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca
APPLICANT: Hitz, William D
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APPLICANT: Cahoon, Rel
APPLICANT: Hitz, Will:
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
                                                             TITLE OF INVENTION: Nucleotide Sequences
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Hitz, William D
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Yadav, Naren
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                                                                                                                                                              Rebecca E
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100.0%; Pred. No.
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6.3e-15;
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                                                                                             New Class of Diverged Delta-9 Stearoyl
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US-10-981-293-24/c

Sequence 24, Application US/10981293 Publication No. US20050066390A1 GENERAL INFORMATION:

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APPLICANT: Yadav, Naren
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR APPLICATION NUMBER: 60/226996
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER: 60/226996
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SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 80
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SOFTWARE: Microsoft Offic
SEQ ID NO 24
LENGTH: 80
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Best Local
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Best Local
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APPLICANT: Cahoon
APPLICANT: Hitz,
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TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS106 and pKS124
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Hitz, William D
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APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THI
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 92
LENGTH: 92
TYPE: DNA
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US-09-887-194A-14
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PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                    FEATURE:
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                          GAGATGACCAGCTCCGGCCG 117
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                                                      Cahoon, Augustian J
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Yadav, Naren
                                                                                                                Conservative
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Pred: No.
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Pred. No.
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US-10-425-115-158821
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SEQ ID NO 158821
LENGTH: 191
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SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 92
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Best Local 9
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
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CURRENT FILING DATE: 2003-04-28
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CCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGA 138
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Lowe, Keith S.
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Pred. No. 27;
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Pred. No.
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                                                                     Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                     TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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LENGTH: 191
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Publication No. US20040123343A1
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE OF INVENTION UNMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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OTHER INFORMATION: Clone ID: MRT4577_76420C.1
                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT4530_16268C.1
                                                                                                                                                                                 ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                        TYPE: DNA
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                                  64
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 CGCCTAGGCTACCGCCGCCACCGCGGCGAGGAGGCCGAATGTCCTGCTGGGGACGATAACA
                                  CGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACT 123
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Barbazuk, Brad
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                                                                       Conservative
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                                                                                     17.8%;
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                                                                                       Score 27.4;
Pred. No. 54
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Pred. No. 27
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                                                      FEATURE:
                                                                                                            ENGTH: 195
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RESULT 20
US-10-437-963-9894/c
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 9894
LENGTH: 175
                                                                                                      NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 31230
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Matches 43; Conserv
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Publication No. US20040123343A1
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Publication No. US20040123343A1
                                                                                                                                           TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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                                       TYPE: DNA
ORĠANISM: Oryza sativa
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OTHER INFORMATION: Clone ID: PAT_MRT4530_35558C.1
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Wu, Wei
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Pred. No. 54;
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RESULT 23
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Publication No. US20040123343A1
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FILE REFERENCE: 00786/350005
CURRENT FILING DATE: 00786/350015
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
                                                                                                                                                                                   APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
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APPLICANT:
APPLICANT:
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EQ ID NO 31230
LENGTH: 195
TYPE: DNA
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Barbazuk, Brad
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Pred. No. 1.4e+
0; Mismatches
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Pred. No. 1.4e+02
0; Mismatches 4
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RESULT 25
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US-09-876-235-34/c
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; OTHER INFORMATION: n =
US-09-876-235-34
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ
SEQ ID NO 34
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 123
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20030022236A1
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
PRIOR PELICATION NUMBER: EARLIER FILING DATE: 1999-02-09
PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
PRIOR PELICATION NUMBER: EARLIER FILING DATE: 1997-11-06
PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
PRIOR PELICATION NUMBER: EARLIER FILING DATE: 1998-01-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 00786/350005
CURRENT APPLICATION NUMBER: US/09/876,235
CURRENT FILING DATE: 2001-06-06
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TITLE OF INVENTION: SELECTION OF
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                          FEATURE:
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15.0%; Pred. No.
tive 26; Mismato
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Pred. No. 2.9e+02;
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; Sequence 34, Application US/10764799 ; Publication No. US20040253612A1

GENERAL

APPLICANT: Szostak, Jack W.

Roberts, Richard W.

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; OTHER INFORMATION: n = a, US-10-764-799-34
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CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/247,190
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: 1997-11-06
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: 1998-01-14
Query Match
Best Local Similarity
Thes 16; Conserv
                                                                                                                                                                              SEQ ID NO 34
LENGTH: 123
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Best Local Similarity 15.0%;
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SEQ ID NO 34
                                                                                                                                                                                                                  NUMBER OF SEQ
SOFTWARE: Fast
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PRIOR APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/247,190
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-21
PRIOR FILING DATE: 1997-01-21
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CURRENT FILING DATE: 2004-01-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
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                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                 Conservative
                                16.2%;
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               Score 25; DB
Pred. No. 2.9e
26; Mismatches
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US-10-029-386-21853/c
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US-10-029-386-21853
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21853, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 21853
LENGTH: 108
                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 21853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HAZEL, DAVID K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENTITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                PILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.0THER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
OTHER INFORMATION: MITHE AF166267.1, EVALUE 2.00e-08
OTHER INFORMATION: MAP TO CHR19.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                  ENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 CAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST_HUMAN HIT: BG122566.1, EVALUE 4.00e-54
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72.7%;
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US-10-767-701-21754/c
; Sequence 21754, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
US-10-767-701-21754
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US-10-767-701-21754
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                                                                                               APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 21754
LENGTH: 167
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Best Local :
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LENGTH: 167
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT FILING DATE: 2004-01-29
UNMBER OF SEQ ID NOS: 63128
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OTHER INFORMATION: E
OTHER INFORMATION: OTHER INFORMATION: S
OTHER INFORMATION: S
                                       ORGANISM: Sorghum bicolor FEATURE:
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                                                                                  TYPE: DNA
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                   OTHER INFORMATION: Clone ID: 13318234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 ATGGTGGAGGCCGCCGCCG 148
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EXPRESSED IN LUNG, SIGNAL = 3.5
EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
NT HIT: AP166267.1, EVALUE 2.00e-08
SWISSPROT HIT: Q05090, EVALUE 3.00e-03
EST_HUMAN HIT: BG122566.1, EVALUE 4.00e-54
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72.7%;
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Pred. No. 3.8e+02;
0; Mismatches 34;
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Pred. No. 3.4e+02;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 167;
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RESULT 32
US-09-923-876-4668/c
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          Sequence 4668, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Lalydd, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 1090-04-01
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR APPLICATION NUMBER: 60/085,331
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PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 4668
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4668, Application US/09923876 Patent No. US20020013958A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lalgudi, Raghunath V. APPLICANT: Kamigaki, Laura Y. (Ito) APPLICANT: Sherman, Bradley K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700455577H1
NAME/KEY: unsure
LOCATION: 150
OTHER INFORMATION: a, t, c, g, or other
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FILING DATE: 1998-05-05
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ilarity 60.6%;
Conservative
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57.0%;
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Pred. No. 4.4e
O; Mismatches
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Pred. No. 3.8e+02
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. 4.4e+02;
tches 26;
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyt
; NAME/KEY: unsure
; LOCATION: 150
; OTHER INFORMATION: a, t,
US-09-923-876-4668
RESULT 34
US-09-923-876-4668/c
; Sequence 4668, Application US/09923876
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 4668
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SEQ ID NO 4668
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Best Local Similarity
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Best Local Similarity
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NAME/KEY: misc feature
OTHER INFORMATION: Incyt
NAME/KEY: unsure
LOCATION: 150
OTHER INFORMATION: a, t,
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Publication No. US20030237110A9
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TYPE: DNA
ORGANISM: Zea mays
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TYPE: DNA
ORGANISM: Zea mays
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Pred. No. 4.4e+02;
0; Mismatches 26;
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Pred. No. 4.4e+02;
0; Mismatches 26;
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US-10-425-115-62701
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SOFTWARE: PERL Program
SEQ ID NO 4668
LENGTH: 164
                                                                                                                        Query Match
Best Local
                                                                                                            Matches
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR PILING DATE: 1998-05-05
NUMBER OF TENEN DATE: 1998-05-05
NUMBER OF TENEN DATE: 1998-05-05
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
TELES REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
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OTHER INFORMATION: Inc:
NAME/KEY: unsure
LOCATION: 150
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ORGANISM: Zea mays
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                                                                                                                        Local Similarity
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Local Similarity 60.6%;
les 40; Conservative
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107 AGCTCCGGCCGCCGACTCGACG 128
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                                              GTCGAG
                                                                           CTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACC 106
                                                                                                          Conservative
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56.1%;
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Pred. No. 4.4e+02;
0; Mismatches 36;
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Pred. No. 4.4e+02;
0; Mismatches 26;
                                                                                                                                         Length 183;
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US-09-864-761-25686
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US-10-425-115-62701/c
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SEQ ID NO 62701
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REPERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic, David K.
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TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                    OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: US 09/632,366
OR FILING DATE: 2000-08-03
OR APPLICATION NUMBER: GB 24263.6
OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR APPLICATION NUMBER: US 60/236,359
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                                                                                                                             APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                           FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                    APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
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                                         APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
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5. US20020048763A1
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Chen, Wensheng
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                    NUMBER: PCT/US01/00665
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l, David K.
2001-01-30
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56.1%;
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Pred. No. 4.4e+02;
0; Mismatches 36;
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US-09-864-761-25686/c
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SOFTWARE: Annous
SEQ ID NO 25686
FRIGHH: 185
                                                                                                                                                                                                                                                                                                     Sequence 25686, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo
FEATURE:
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                    APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
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N: EXPRESSED IN ADULT LIVER, SIGNAL =

N: EXPRESSED IN PETAL LIVER, SIGNAL = 7.

N: EXPRESSED IN PLACENTA, SIGNAL = 7.

N: EXPRESSED IN BAAIN, SIGNAL = 6.7

N: EXPRESSED IN HEART, SIGNAL = 6.7

N: EXPRESSED IN HEARIN, SIGNAL = 6.7

N: EXPRESSED IN HEARIN, SIGNAL = 8.6

N: EXPRESSED IN HEARIN, SIGNAL = 8.6
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US 09/632,366
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Pred. No. 4.4e
0; Mismatches
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ADULT LIVER, SIGNAL
FETAL LIVER, SIGNAL
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.4e+02;
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APPLICATION NUMBER: US 60/236,359

2000-10-04 UMBER: US 2000-09-27

FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6

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RESULT 39
US-10-753-646-15
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
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SOFTWARE: Annomax Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 185
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                        100 TGCCCACTACGCCGATGGAGGAGATGGACAGCTGCGCGCAGGGCTCGGTGGACCCCGCTCA
                                                                                                                                                                                                                                                                                                                                160 CTAGCTCCTTGGTGAGAAACTCAAAGAAGTGGGCGCTGTGGCTGCGGTTGTCCTCGGCGG
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                                                                                                                                                GCGCCATGGCCAGGCCCGGCCG 19
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llarity 53.5%;
Conservative
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DN: EXPRESSED IN ADULT LIVER, SIGNAL = 9.4

DN: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4

DN: EXPRESSED IN FETAL LIVER, SIGNAL = 7.6

DN: EXPRESSED IN BONE MARROW, SIGNAL = 15

DN: EXPRESSED IN HEART, SIGNAL = 5.6

DN: EXPRESSED IN HEART, SIGNAL = 6.7

DN: EXPRESSED IN HELA, SIGNAL = 8.6

DN: EXPRESSED IN HELA, SIGNAL = 8.6

DN: NT HIT: AP240786.1, EVALUE 1.00e-100

DN: SWISSPROT HIT: P30046, EVALUE 8.00e-28

DN: EST_HUMAN HIT: AV655183.1, EVALUE 1.00e-100
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Pred. No. 4.4e+02;
0; Mismatches 61;
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APPLICANT: DAVIDSON, DONAID J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: 5940.US.P3
CURRENT APPLICATION NUMBER: US/10/753,646
CURRENT FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US/08/924,287A
PRIOR FILING DATE: 2004-01-08
PRIOR PRILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: US 08/851,350
PRIOR APPLICATION NUMBER: US 08/851,350
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/832,087
                                                                        ; FEATURE: ; OTHER INFORMATION: Synthetic DNA Fragment US-10-753-646-15
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US-10-753-646-15/c
US-10-753-646-15/c
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
; GENERAL INFORMATION:
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US-10-753-646-15
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CURRENT FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US/08/924,287A
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US 08/851,350
PRIOR PILING DATE: 1997-05-05
PRIOR PPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/643,219
PRIOR APPLICATION NUMBER: US 08/643,219
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LENGTH: 175
                                                                                                                                                                                                                        SEQ ID NO 15
Query Match
Best Local Similarity
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Best Local 9
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APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: 5940.US.P3
                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/643,219
PRIOR FILING DATE: 1996-05-03
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                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
Local Similarity 62.3%;
nes 38; Conservative
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Pred. No. 5.1e+02
0; Mismatches 2:
Score 24.2; DB 18;
Pred. No. 5.1e+02;
                                                                                                synVB2
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                       Length 175;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 140476
LENGTH: 183
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US-10-425-115-140476
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US-10-425-115-140476/c
Sequence 140476, Application US/10425115
; Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59598C.1
US-10-425-115-140476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 140476, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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LENGTH: 183
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(183)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(183)
                                       FEATURE:
                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 G 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 GCCGACTCGACGATGAGC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGGACTCGACGATGAGCGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 CGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACCATGGCCACCGGGGCCGACAACCGCGACGGCATGGGCTACCAGACCCGCGNCGGGC
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56.4%;
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Pred. No. 5e+02;
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; OTHER INFORMATION: Clone ID: MRT4577_59598C.1
US-10-425-115-140476
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US-10-156-761-3130
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US-10-156-761-3130/c
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3130
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3130, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
                                                                                                                                                                 Sequence 3130, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                  APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (1)..(192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                        104 TOGGGTTCTATCTCGCGTCCTCGACCGTCGCCCCGACCATCAACGAGCTGACGA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GCGCGTCGGCGAGTCGGAGCCCGNCGCGGGTCTGGTAGCCCATGCCGTCGCGGTTGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                              54 TCTCGCTCATCGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCA 107
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HORIKAWA, HIROSHI
                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23.6; DB 15;
Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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APPLICANT: LA ROSS, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 22757
LENGTH: 155
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(155)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3130
LENGTH: 192
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (11..(192)
US-10-156-761-3130
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US-10-425-115-22757
; Sequence 22757, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Search completed: April 9, 2005, 02:42:41
Job time : 498 secs
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; OTHER INFORMATION: Clone ID: MRT4577_120756C.1
US-10-425-115-22757
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Best Local Similarity 50.0%;
Matches 42; Conservative
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                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 TCGTCAGCTCGTTGATGGTCGGGGGGGACGCTCGAGGACGCGAGATAGAACCCGA 104
                                                                                                                         123 TCGACGATGAGCGAGATGACCAGC 146
                                                                                                                                                                     57 TCGTCGACCGGGGGGGGGGAAAGCNCNNCCACTAAGNNTNCAACCTCCNNCCGNTGAA 116
                                                                                                                                                                                                             48 TGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGA 101
                                                                                   GCGACAGNGCCGAAGCGAAGGAAC 140
                                                                                                                                                                                                                                                   Score 23.4; DB 18;
Pred. No. 8.9e+02;
0; Mismatches 42;
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Result
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154
1 cggccggagctggtc:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Maximum Match 100%
Listing first 100 :
    cggccggagctggtcatctc.....
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US-09-513-999C-13979

US-09-521-976-19276

US-09-621-976-19276

US-09-621-976-19276

US-09-621-976-19276

US-09-619-670-3

US-09-947-190-34

US-09-947-190-34

US-09-913-999C-16612

US-09-913-999C-16612

US-08-913-999C-16612

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US-08-924-287A-15

US-08-924-287A-15

US-08-924-287A-15

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## ALIGNMENTS

RESULT 1 US-09-313-294A-6653

Application US/09313294A

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte I
; NAME/KEY: unsure
; LOCATION: 108, 196
; OTHER INFORMATION: a, t, c,
US-09-313-294A-6653
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SEQ ID NO 6653
LENGTH: 197
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Patent No. 64762
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APPLICANT:
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                        APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILLING DATE: 1999-05-14
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SOFTWARE: PERL Program
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700352170H1
NAME/KEY: unsure
LOCATION: 108, 196
OTHER INFORMATION: a, t, c, g, or other
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TYPE: DNA
                                                                                                        FEATURE:
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Ito, Laura Y.
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US-09-513-999C-13979/c; Sequence 13979, Appl

Application US/09513999C

Patent No. 6783961;
GENERAL INFORMATION:
APPLICANT: Dumas Mil
APPLICANT: Duclert,

Dumas Milne Edwards, J.B

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RESULT 4
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Best Local Similarity
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SOFTWARE: Patent.pm
SEQ ID NO 13979
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 57
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LOCATION: 9
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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OTHER INFORMATION: 8=9
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Pred. No. 2e+02;
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Pred. No. 4.5e+02;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ESTS and Encoded Human FILE REFERENCE: GENSET.054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NO 19276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19276, Appearent No. 6639063
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Best Local Similarity
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SOFTWARE: Patent.pm
SEQ ID NO 13979
LENGTH: 195
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins atent No. 6783961
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                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 11
OTHER INFORMATION: n=a,
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LOCATION: 9
OTHER INFORMATION: s=g
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                                                                                                                                                                                                                                                      ENGTH:
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                                                                                                                                              Match 17.0%;
Local Similarity 55.1%;
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                                                                                                                                  49; Conservative
                                CGAGATGACCAGCTCCGGCCGCCGACTCG 125
CTACGTCCCCAGCTCCAGCCGCCGGMTCG 135
                                                                GCTGCGGCGGTGTCTCGCGTTCGGCGGGATTTCTCTTCGCTCCGGCTCGGCCTAGGT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCGAACGCGAGACACYGCCGCCGCAGC 46
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                                                                                                                                Score 26.2; DB 4;
Pred. No. 5.7e+02;
1; Mismatches 39;
                                                                                                                                  1; Mismatches
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Pred. No. 4.5e+02;
0; Mismatches 39;
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; ORGANISM: Homo sapiens
US-09-621-976-19276
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US-09-621-976-19276/c
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SOFTWARE: Patent.pm
SEQ ID NO 19276
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/621,976
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TITLE OF INVENTION: ESTs and Encoded Human Proteins
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,670
FILING DATE: 09-MAR-1998
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                                                                                            APPLICATION NUMBER: PCT/FR96/00: PILING DATE: 31-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06578
FILING DATE: 02-JUN-1995
                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: PCT/FR96/00821
                                                                          FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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NAME: Granados, Patricia D.
REGISTATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 065691/0128
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20007-5109
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3000 K Street, N.W., Suite 500
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55.1%;
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Pred. No. 5.7e+02;
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                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                APPLICATION NUMBER: PCT/FR
FILING DATE: 31-WAY-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR 95/
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
MOLECULE TYPE:
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           FILING DATE: 09-MAR-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                      NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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APPLICATION NUMBER: US
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APPLICANT:
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CITY: Washington
                 TOPOLOGY:
                             STRANDEDNESS:
                                                                                                                           TELEFAX:
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Local Similarity 59.7%;
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                                             nucleic acid
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                                                                                                                           (202) 672-5399
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Pred. No. 8e+02;
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29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 123
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Best Local (
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Patent No. 62010.
Patent INFORMATION:
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Best Local Similarity
                                                           TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350005 CURRENT APPLICATION NUMBER: US/09/247,190 CURRENT FILING DATE: 1999-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
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APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-01-21
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
                                                   BARLIER
                                                                                                                                             APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
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CURRENT APPLICATION NUMBER: UCURRENT FILING DATE: 1999-02-
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ORGANISM: Homo sapiens
FEATURE:
                                ARLIER
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APPLICATION NUMBER: 60/064,491 FILING DATE: 1997-11-06
                              APPLICATION NUMBER: 60/035,963 FILING DATE: 1997-01-21
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Pred. No.
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Pred. No. 8
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LENGTH: 123
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                             PATENT NO. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6783961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16612, Application US/09513999C Patent No. 6783961
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-09-513-999C-16612
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PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
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EARLIER FILING DATE: 1998-01-14
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SOFTWARE: Patent.pm
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FILE REFERENCE: 59.US2.REG
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SOFTWARE: FastSEQ for Windows Version 4.0
TUMBER OF SEQ ID NOS:
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Local Similarity 15.0%;
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Similarity 67.3%;
35; Conservative
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Pred. No. 1.3e+03;
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Pred. No. 1.1e+03;
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                                                                                                                              US-08-851-350-15
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LENGTH: 181
                                                              Query Match
Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
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OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,3:
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patent.pm
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                          NAME: Casuto, Dianne REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                            TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGG
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Abbott Park
 CATCACGGTGGTGGTGCCGCGCGCGCAGCTGAAGAGCTGGCTCACCTTCGGGTGGG
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                                                                                                                                                                                          175 base pairs
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/ENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
/ENTION: POLYNUCLECTIDES ENCODING SAME AND METHODS
//ENTION: FOR INHIBITING ANGIOGENESIS
                                                               Conservative
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                                                                                                                                               linear
                                                                               15.7%;
62.3%;
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                                                              Score 24.2; DB 3;
Pred. No. 1.8e+03;
0; Mismatches 23;
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Pred. No. 1.3e+03
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                                                                                          Length 175;
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RESULT 15
US-08-924-287A-15
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US-08-851-350-15/c
                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                  Sequence 15, Application US/08924287A Patent No. 6699838
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity 62.3%;
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GENERAL INFORMATION:
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                 CURRENT APPLICATION NUMBER: US/08/924,287A CURRENT FILING DATE: 1997-09-05
                                                   APPLICANT: Abbott Laboratories
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: 5940.US.P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,3/
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Casuto, Dianne 40,943
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
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APPLICATION NUMBER:
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NVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
NVENTION: POLYNUCLBOTIDES ENCODING SAME
NVENTION: FOR INHIBITING ANGIOGENESIS
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US 08/851,350
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Pred. No. 1.8e+03;
0; Mismatches 23;
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US-08-924-287A-15/c
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08924287A
Patent No. 6699838
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNICLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
TITLE OF INVENTION: ANGIOGENESIS
                                                                                                                                        Matches
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 175
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/08/924,287A
CURRENT FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 08/851,350
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/643,219 PRIOR FILING DATE: 1996-05-03
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PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/643,219
                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic DNA Fragment synVB2
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                                                                                                                                                      Local
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31 G 31
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                                                                                                                                      l Similarity
38; Conserv
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Pred. No. 1.
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Pred. No. 1.8e+03;
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                                                                                                                                      Mismatches
                                                                                                                                                      .8e+03
                                                                                                                                                                      DB 4;
                                                                                                                                                                     Length 175;
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RESULT 17 US-09-513-999C-15749 ; Sequence 15749, Application US/09513999C

INFORMATION:

Edwards,

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; LOCATION: 45
; OTHER INFORMATION: 8=g or c
US-09-513-999C-15749
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 15749
LENGTH: 71
                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 15749
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
                                                    Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                         LENGTH: 71
TYPE: DNA
                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 35
OTHER INFORMATION: r=a
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NAME/KEY: misc_feature
                                                                                                                                               NAME/KEY: misc_feature
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OTHER INFORMATION: r=a or
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LOCATION: 45
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                                Local Similarity
es 35; Conserv
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27 CGTCGAGTCGGCGGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCC 82
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                                  Conservative
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                                1; Mismatches
                            Score 23.6; DB 4;
Pred. No. 2.4e+03;
Nismatches 20;
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Pred. No. 2.4e+03;
1; Mismatches 20;
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                                                              Length 71;
                                Indels
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; ORGANISM: Myxococcus xanthus
US-09-902-540-8568
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US-09-902-540-8568/c
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; ORGANISM: Myxococcus xanthus
US-09-902-540-8568
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US-09-902-540-8568
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8568
LENGTH: 195
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SEQ ID NO 8568
LENGTH: 195
                                                                                                                                       Matches
                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8568, Application US/09902540 Patent No. 6833447
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                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILLING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome
FILE REFERENCE: 38-10(1.5849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 41; Conserv
 102
                                 137 GATGACCAGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 GCTCGGCGCC 162
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                                                                                                                                       41;
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                                                                                                    GCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGA 136
GACCGCCAGC
                                                                   GGCGCCGAGCCGCAGCCGCGCCTTGCGCCGCGTCCGCGCCCTCCGCGTCGACCGC 103
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                                                                                                                                       Conservative
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58.6%;
93
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Pred. No. 2.5e+03;
                                                                                                                                     Score 23.6; DB 4;
Pred. No. 2.5e+03;
0; Mismatches 29;
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                                                                                                                                                                      Length 195;
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RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2996
LENGTH: 126
TYPET - NUM
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Tocal Similarity
                                                                                                                                                                                                                                           Matches
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LENGTH: 126
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                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Myxococcus xanthus -09-902-540-2996
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                               ocal
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5. 6833447
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                                                                                                                  62 ATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGC 109
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                                                                                                                                                                                               1 Similarity
55; Conserv
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                                                                                                                                                           GCCCACAGCTCGCGCGTGGCCTCATTCTCGCGTTGACGGGTTGACGGGCGTCTGGATGCCC
                                                                            ATCAGCGCCGCGGCGAGCAGGATGGACGATGGCCACCGTGACCATC 3
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                                                                                                                                                                                                                                                           15.1%;
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Pred. No. 3.1e+03;
0; Mismatches 53;
                                                                                                                                                                                                                                                         Score 23.2; DB 4;
Pred. No. 3.1e+03;
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                          DB 4;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-447-985-14
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Patent No. 6399861
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: DEKM:055/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 713/789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,985
FILING DATE: 23-May-1995
                                                                                                                                                                                APPLICANT: Adams, Thomas R. et al.
TITLE OF INVENTION: Methods and Compositions for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/113,561
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adams, Thomas R. et al.
TITLE OF INVENTION: Methods and Compositions for the
Production of Stably Transformed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                       NUMBER OF SEQUENCES:
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ADDRESSEE: Arnold, White & Durkee
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NUMBER OF SEQUENCES: 26
CORRESPONDENCES 26
                                                                                                                                                                                                                                                                                                                                                                     110 CÉCCAGCCTCCCCGTCG 126
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43; Conserv
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                 CITY: Houston
STATE: Texas
                                                         STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Texas
COUNTRY: USA
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                                                                                                                                                           Production of Stably Transformed,
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Pred. No. 4.5e+03;
0; Mismatches 34;
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                                                                                                                                                             Fertile Monocot Plants
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
APPLICATION NUMBER: US/08/852,340
FILING DATE: 07-MAY-1997
CLASSIFICATION DATA:
APPLICATION UMBER: US 07/113,561
PRIOR APPLICATION DATA:
APPLICATION US/08/852,340
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                      CITY: Houston
STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,985
FILING DATE: 23-M8y-1995
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 08/113,561
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: DEKM:055/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 CGACGGGGAGGCTGGCGGTGGACTTGAGCCCCTGGAACGGAGCGACGGCGGTGGCCGACG 67
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, Thomas R., et al.
VENTION: METHODS AND COMPOSITIONS FOR THE
VENTION: PRODUCTION OF STABLY TRANSFORMED,
VENTION: AND CELLS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                         Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08852340
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Query Match
Best Local Similarity
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/113

FILING DATE: 25-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: DEKM

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,340
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Adams, Thomas R., et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: PRODUCTION OF STABLY TRANSFORMED,
TITLE OF INVENTION: AND CELLS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                    STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Houston
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lir
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                                                                                               nucleic acid
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                                                                                                                                                                         : (512) 418-3000
(713) 789-2679
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                                                                      linear
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25-AUG-1993
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14.7%;
55.8%;
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Pred. No. 4.5e+03;
Score 22.6; DB 4;
Pred. No. 4.5e+03;
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                Length 185;
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US-08-622-740-9/c
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                                                                             RESULT 28
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              Sequence 9, Application US/08622740
Patent No. 5990390
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                        Query Match
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    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/
FILING DATE: 27-MARCH-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lundquist, Ronald C. APPLICANT: Walters, David A. APPLICANT: Kirihara, Julie A.
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                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 95
                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Minneapolis
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                                                                                                                       104 AGGGGCTCAAGTCCACCGCCAGCCTCCCCGTCG 136
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                                                                                                                                                                                   44
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                                                                                                                                                                                                                                                          Similarity
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Lundquist, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                        14.7%;
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                                                                                                                                                                                                                                          Score 22.6; DB 2;
Pred. No. 4.5e+03;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                        950.013US4
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                                                                                                                                                                                                                                                                     Length 195;
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US-08-440-689-9
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                                                                                                                                                                                                                                                                                                                                        Patent No.
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                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,740
FILING DATE: 27-MARCH-1996
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.013US4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Walters, David A.
APPLICANT: Kirihara, Julie A.
APPLICANT: Kirihara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fe
TITLE OF INVENTION: and Cells Thereof
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: 3500 IDS Center
                                                                                                         CITY: Minneapolis STATE: MN
 OPERATING SYSTEM:
                                                                      COUNTRY: U
                                                                                                                                             STREET:
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STRANDEDNESS: single
                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 CGACGGGGAGGCTGGCGGTGGACTTGAGCCCCTGGAACGGAGCGACGGCGGTGGCCGACG 77
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49; Conserv
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3500 IDS Center
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COMPATIBLE
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%;
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Methods and Compositions for the

Production of Stably Transformed, Fertile Monocot Plants
                                                                                                                                                           Lundberg, Woessner & Kluth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9:
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Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 195;
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US-08-440-689-9/c
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TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: mucleic acid
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Best Local Similarity 52.7%;
Matches 49; Conservative
                                                                                                                                     TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
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                          SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,689
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WOESSNEY, WARTEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 95C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,689
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
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LENGTH: Locality and the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                             TELEPHONE:
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3500 IDS Center
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Kirihara, Julie A.
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Pred. No. 4.5e+03;
0; Mismatches 44;
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Best Local Similarity
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/122,399
FILING DATE:
                                                                                                                                                                                                                                                                               TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-AUG-1993
ATTORNBY/AGENT INFORMATION:
NAME: WOESSHEY, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
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APPLICANT: Walters, I
APPLICANT: Kirihara,
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APPLICATION NUMBER: 1
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TITLE OF INVENTION:
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                                                                                                                                                                                             TYPE:
STRANDEDNESS: SIL
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                                                                                                                                       Local Similarity
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104 AGGGGCTCAAGTCCACCGCCAGCCTCCCCGTCG 136
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                           96 GCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
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                                                                                                                         Conservative
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52.7%;
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Pred. No. 4.5e+03;
0; Mismatches 44
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                                                                                                                                      Score 22.6; DB 3;
Pred. No. 4.5e+03;
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US-08-440-646A-9
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                                                                                                                     Sequence 9, Application US/08440646A Patent No. 6777589
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Kirihara, Julie A.
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 30,440
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ZIP: 55402
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Kirihara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed, and Cells Thereof
NUMBER OF SEQUENCES: 22
                                                                                                     APPLICANT: Lundquist,
                                                                                                                                                                                                                                                                                                              136 CGACGGGGAGGCTGGACGTTGAGCCCCTGGAACGGAGCGACGGCGGTGGCCGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/112,245
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                                                                                                     Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                              Score 22.6; DB 3;
Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        950.13US01
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 195;
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                                 Fertile Monocot Plants
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US-08-440-646A-9/c
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,646A
FILING DATE: 15-May-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, L
STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                                   Kirihara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-331
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lu
STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 AGGGGCTCAAGTCCACCGCCAGCCTCCCCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 GGCGGCCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 GCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                   COUNTRY: USA
ZIP: 55402
                                                                                                                                                             STATE: MN
                                                                                                                                                                              CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGCCCACCGTGATGAACCGTGATGATGGCCTCGTCGGCCACCGCCGTCGCTCCGTTCC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MN
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52.7%;
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Pred. No. 4.5e+03;
0; Mismatches 44;
                                                                                                                                                                                                                       Lundberg & Woessner, P.A
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                   Version #1.25
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RESULT 35
US-08-105-168B-6
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                                                                     CURRENT APPLICATION DATA:
FILING DATE: AUGUST 12, 1993
APPLICATION UMBER: US/08/105,168B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: AUGUST 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TELEPHONE: (703) 836-6400
TELEPAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: 01iff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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STATE: V1.
22314
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OPERATING SYSTEM:
SOFTWARE: Wordper
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LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
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FILING DATE: 25-AUG-1993
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 CGACGGGGAGGCTGGCGGTGGACTTGAGCCCCTGGAACGGAGCGACGGCGGTGGCCGACG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Woessner, Warren D. REGISTRATION NUMBER: 30,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia
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                                                                                                                                                                                                                                                                                                                                                 IBM compatible SYSTEM: MS DOS 3.1
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52.7%;
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Pred. No. 4.5e+03;
0; Mismatches 44;
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TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Applicati
Patent No. 5589585
GENERAL INFORMATION:
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Best Local Similarity 57.1%;
                                                                                                                APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
AȚTORNEY, AGENT INFORMATION:
NAME: William P. Bezridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
FILING DATE: August 12, 1993
APPLICATION NUMBER: US/08/105,168B
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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ANTI-SENSE:
ORIGINAL SOURCE:
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STATE: V11
22314
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OPERATING SYSTEM: MS
SOFTWARE: Wordperfect
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IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 700 South CITY: Alexandria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: 81
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOSOME/SEGMENT:
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single-stranded
                                                                                                                                                                                                                                                                                                                                                                                               MS DOS 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMERS, HYBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION POR THE DETIPIERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Pred. No. 4.5e+03;
                                                                                                                                                         28835
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US-08-698-948-6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MABILA
                                                                                                                                                        FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
                  TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
                                                                                               REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WFB 28835A
TELECOMMUNICATION INFORMATION:
77031 836-6400
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948
FILING DATE: August 16, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: POSITION IN GENOME: CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Mycobacterium intralcellulare
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM con
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP POSITION:
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                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 TGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CGGTGGCAGCGATCTGGTCCTTGGTCTCGACCTCCTTGGCCGACTTGAGCAGGGTCTCGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 CGGAGCTGGTCATCTCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08698948
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MABILAT et al.
                200 base pairs
                                                                     : (703) 836-64
(703) 836-2787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%;
                                                                                       836-6400
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                                                                                                                                                                                                                                                                                                                                                                                                MS DOS 3.1
                                                                                                                                                                                                                FR9210094
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Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels
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                   TELEFAX: (703) 836-27
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: August 16,
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MABILAT et al.

TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETI-
TITLE OF INVENTION: MYCOBACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                            APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,1
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS
SEQUENCE CHARACTERISTICS:
                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VIII
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Local Similarity 57.1%;
hes 60; Conservative
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single-stranded
                                                                                           NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible OPERATING SYSTEM: MS DOS 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 700 South Washington CITY: Alexandria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium intralcellulare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 518-717
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, Application US/08698948
5. 5849901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia
                                       (703)
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                                                                                                                                                                                                                                                                                             August 16, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                    3.5" DS/HD
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Pred. No. 4.5e+03;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Street,
                                                                                             28835A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
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nucleic acid

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RESULT 40

US-09-902-540-8045/c

; Sequence 8045, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:
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US-09-902-540-8045
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NO 8045
LENGTH: 174
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                     Query Match 14.5%;
Best Local Similarity 59.4%;
Matches 38; Conservative
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Patent No. 6833447
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Best Local Similarity 57.1%;
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intralcellulare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                    159
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                                                                                                                                    GAAG 162
                                                                                                                                                                                                           GCCGCGGCCGCGCCCCCCGCTATTCGGCGAGCTGCAGGCCGCCTACGAGAAGGCGCTGGT 158
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                                                                                                                                                                                                                                                                                   Score 22.4; DB 4; Length 174; Pred. No. 5e+03; O; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22.6; DB 2;
Pred. No. 4.5e+03;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
FILE OF INVENTION: Myxococcus xanthus Genome Second Reference: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8045
LENGTH: 174
                                                                                           RESULT 42
US-09-902-540-7303/c
                                                                                                                                                                                                                                                                                                                                                          ; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7303
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7303
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; ORGANISM: Myxococcus xanthus
US-09-902-540-8045
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                                             Sequence 7303, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7303, Applic Patent No. 6833447 GENERAL INFORMATION:
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Best Local (
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 39-10(15849)B
CURRENT FILINGIATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
APPLICANT: Goldman,
APPLICANT: Hinkle,
APPLICANT: Slater,
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                                                                                                                                                                                                                                                                                               Conservative
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Gregory J. Steven C.
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Pred. No. 5e+0
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Pred. No. 6.1e+03;
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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7303
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                                                                                  RESULT 44
US-09-313-294A-6924/c
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7333
               Sequence 6924, Application US/09313294A
Patent No. 6476212
GENERRAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
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Patent No. 6476212
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APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
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APPLICANT:
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OTHER INFORMATION: Incyte ID No. 6476212 700380851H1
NAME/KBY: unsure
LOCATION: 22, 60, 64, 76, 83, 85
OTHER INFORMATION: a, t, c, g, or other
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Ito, Laura Y.
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Sequence 8725, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sec.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR TILING DATE: 2000-07-10
PRIOR TILING DATE: 2000-07-10
PRIOR TILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8725
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US-09-902-540-8725
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Search completed: April Job time : 133 secs
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION UNUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
UNUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6924
LENGTH: 164
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Best Local (
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OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 22, 60, 64, 76, 83, 8
OTHER INFORMATION: a, t, c, g,
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                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Myxococcus xanthus
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Local Similarity 48.6%;
nes 52; Conservative
                                                                                                                                                                                                                                                            Local Similarity
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nilarity 49.2%;
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DB seq length: 200
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                                                     The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the
  complements
                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                    New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
                                                                                                                                                                                                           Claim 45; Page 37; 77pp;
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Nichols SE;
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PIONEER HI-BRED INT INC.
                   constructs are also used in reducing expression of a target similar endogenous mRNA. The sequences and their reverse
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Best Local
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Nichols SE;
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                                                                                                           2002-139927/18.
DB; AAE18333.
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New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a tamRNA and its reverse complement unrelated to endogenous DNA, for redu

a target reducing

expression

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 2X ELVISLIVES complementary repeat region DNA found in plasmid pKS133 used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the
                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                Plasmid pKS133
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD32908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD32908 standard; DNA; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 154
22-AUG-2000; 2000US-0226996P
                          22-AUG-2001; 2001WO-US026246
                                                                                 WO200216565-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 45; Page
                                                                                                                                                                                                                                                                                                                                         transgenic
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                                                                                                                                                                                                                                                                                                                                      diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                2X ELVISLIVES complementary repeat DNA
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                  product=
                                                                                                                                                                                                                               product= "ELVISLIVES protein"
                                                                                                                                                                             omplement (82.
                                                                                                                                                                                        product= "ELVISLIVES
                                                                                                                                    product= "ELVISLIVES
omplement(119. .148)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to a new recombinant construct.
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                                                                                                         "ELVISLIVES protein"
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Pred. No. 2.7e-28;
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proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-initing, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the golypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce is IX ELVISLIVES complementary repeat region DNA found in plasmid pKS133 This sequence is used in the exemplification of the invention for the
                  Query Match
Best Local (
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, po- and unsaturated fatty acids and in increasing the unsaturation levels
                                                                            Sequence 154 BP; 24 A; 53 C; 53 G; 24 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in cellular lipids.
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                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to diverged delta-9 fatty acid desaturase
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  154;
                  Similarity
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                                                                                                                    of Fad2 in soybean
  Conservative
                100.0%;
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                Score 154; DB 6;
Pred. No. 2.7e-28;
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                oil; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
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                                                                                                                                                                                                                                                                                                     Unidentified
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44. .74
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                                                                                       "ELVISLIVES protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme; cellular lipid;
tion; plasmid pKS133; ge
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 154
                                                                                                                                                                                                                                                                                                                                                                                                                     suppression of Fad2 in soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 43; 77pp; English.
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                                                             standard; DNA; 154 BP
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(first entry)
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complement(82. .111)
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/product= "ELVISLIVES protein"
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Pred. No. 2.7e-28;
; Mismatches 0;
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Seed specific gene silencing vector pKS151, stem loop region
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pKS151; seed specific promoter; gene silencing; chalcone reductase; transgenic; liquiritigenin-derived isoflavone; isoflavoned; food product; snack food product; baked good product; fried food product; fried food product; infant formula; beverage; nutritional suppleme dairy product; pet food product; animal feed; ss. nutritional supplement; fried food product;

Synthetic

stem\_loop /\*tag= Location/Qualifiers

US2004128714-AJ

01-JUL-2004

11-DEC-2003; 2003US-00734947

13-DEC-2002; 2002US-0433433P

WPI; 2004-533136/51

Decreasing ratio of liquiritigenin-derived isoflavones relative to tot isoflavones in a plant comprises transforming plant cell with nucleic acid sequence showing homology to sequence encoding chalcone reductase (deoxychalcone synthase). total

Example 7; SEQ ID NO 7; 25pp; English.

The invention relates to decreasing the ratio of liquiritigenin-derived construct comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct to ADQ07965 (a soybean chalcome reductase cDNA). Also included correct an isoflavonoloproducing plant made by the method above, seeds or company a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels obtained from the seeds or plant parts, a construct of the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product, and a method of convoluting an isoflavonoid-containing product, and a method of convoluting an isoflavonome relative to the total isoflavone convolution of liquiritigenin comprises a stem-loop structure. The nucleic acid sequence forms a loop in the stem-loop structure and the component of the methods and recombinant construct are useful in correct is a seed-specific producing an isoflavones relative to the total isoflavone in an isoflavone-convolution plant. The methods and recombinant construct are useful in correct health food product, infant formula, baked good product, fried food correal food product, infant formula, baked good product, fried food correct infant formula. product, health food product, infant formula, beverage, nutritional supplement, dairy product, pet food product, or animal feed. The prosequence is the single stranded version of the stem loop region from plasmid pKS151. The present

Sequence 154 BP; 24 A; 53 c; 53 **.** 24 T; 0 U; 0 Other;

맑 Ś Query Match Best Local S Matches 154 154; Similarity CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 100.0%; 0 Score 154; DB 12; Pred. No. 2.7e-28; Mismatches 0; Length 0 60 60 0

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RESULT 6
ADQ07968/c
ID 007968;
XX ADQ07968;
XX ADQ07968;
XX Seed specific gene s
XX Seed specific gene s
XX PKS151; seed specific
XW transgenic; liquirit
XW pKS151; seed specific
XW pKS151; seed specific
XW pKS151; seed specific
XW pKS151; seed specific
XX pCS151, seed specific
XX pCS151, seed specific
XX pKS151; seed specific
XX pKS151; seed specific
XX pCS151, seed specific
XX pKS151; seed specific
XX pCS151, seed specific
XX Local production
XX pCS151, seed specific
XX pCS151, seed specif
The invention relates to decreasing the ratio of liquiritigenin-derived construct comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct to ADQ07965 (a soybean chalcone reductase cDNA). Also included core in isoflavonoid-producting plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product construing a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels obtained from the seeds or plant parts, a concorporated the isoflavonoid-containing product, and a method of concorporated the isoflavonoid-containing product, and a method of concorporated isoflavonoid-containing product having a reduced ratio of concorporated isoflavonoid-containing product having a reduced ratio of concorporated sequence forms a loop in the stem-loop structure. The stem comprises a sequence of ADQ07968). The promoter is a seed-specific componer. The method is useful for decreasing the ratio of liquiritigenin construct and the second plant. The methods and recombinant construct are useful in producting an isoflavonoid-containing product which is incorporated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Decreasing ratio of liquiritigenin-derived isoflavones relative to total isoflavones in a plant comprises transforming plant cell with nucleic acid sequence showing homology to sequence encoding chalcone reductase
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transgenic; liquiritigenin-derived isoflavone; isoflavonoid;
food product; snack food product; baked good product; fried food product;
health food product; infant formula; beverage; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; SEQ ID NO 7; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2003; 2003US-00734947
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1. .154
/*tag= a
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RESULT 7
ABK10711
ID ABK10711
AC ABK1
XX ABK1
XX ABK1
XX Plas

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Best;Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cereal food product, snack food product, baked good product, fri product, health food product, infant formula, beverage, nutritio supplement, dairy product, pet food product, or animal feed. The sequence is the single stranded version of the stem loop region plasmid pKS151.
                                                                                           Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                                                                                               WPI; 2002-156692/21.
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                                                                                                                                                                                                                                                                                                                                                                               17-JUL-2000; 2000US-0218712F
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                                                                                                                                                                                                     P-PSDB; AAU77109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "No start or stop codon shown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "ELVISLIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                start or stop codon shown"
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Example

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Page 19;

27pp; English

levels.

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RESULT 8
ABK10711/c
ID ABK107
XX ABK107
XX ABK107
XX ABK107
XX O5-JUN
XX Plasti.
XX Plas
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Best Local
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                                                                                                                                                                        17-JUL-2001; 2001EP-00306143
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                                    (DUPO ) DU PONT
                                                                                                                                                                                                                                                  23-JAN-2002.
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                                    DE NEMOURS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        product= "ELVISLIVES peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        partial
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100.0%; Pred. No.
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   "No start or stop codon shown'
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hes 0;
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Matches
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WO200200904-A2
                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                    Recombinant construct; gene
                                                                                                                                                                                                                                                      Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA
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                                                                                                                                                                                                                                                                                                                                                       AAD29230 standard; DNA; 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGATGACCAGCTCCGGCCG
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                                              /product= "ELVISLIVES protein"
complement(45. .74)
/*tag= b
                                                                                                                                 Location/Qualifiers
                               /product= "ELVISLIVES protein"
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                                                                                                                                                                                                                                                                                                                                                         Β₽
                                                                                                                                                                                                                  expression; plasmid pKS124; plasmid pKS106;
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Pred. No.
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22

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RESULT 10
AAD29230/c
ID AAD29230 standard; DNA; 80 BE
XX
AC AAD29230;
XY
OT 07-MAY-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X EE
XX
AC ACCOMMINATION CONSTRUCT; gene 6
XX
COS Unidentified.
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COS Unidentified.
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COS Unidentified.
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COS Unidentified.
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COS COMPLETE a
FT CDS /*tag= a
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FT CDS Complement (4:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target
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P-PSDB; AAE18333.
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PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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llarity 100.0%;
Conservative
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 /*tag= a
/product= "ELVISLIVES protein"
complement(45. .74)
                                                                 Location/Qualifiers
                                                                                                                                                                         pKS124 1X ELVISLIVES
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                                                                                                                                            expression;
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                                                                                                                                                                         complementary repeat DNA.
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hes 0;
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                                                                                                                                          plasmid pKS124; plasmid pKS106;
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Best Local
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106 and pKS124 used in the exemplification of the
                                      Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pKS124; plasmid pKS106; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant construct having a promoter operably linked to a sequence which when expressed produces an RNA having homology to mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glassman KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001; 2001WO-US019962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200200904-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000; 2000US-0213961P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 45; Page 37;
                                                                                               Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
                                                                                                                           01-JUL-2002
                                                                                                                                                                                    AÁD32907 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
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DB; AAE18333.
                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                80
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                                                                                                                                                                                                                                                                                                                                                                      80;
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                               GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                                                                                                                          GAGATGACCAGCTCCGGCCG 1
                                                                                                                                                                                                                                                                                                                CGGCCGGAGCTGGTCATCTCGTCGATCGTCGAGTCGGCCGCCGACTCGACGATGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon-Kamm WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                             12
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                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                             A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                             28 C;
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                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 6; L
Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinney
                                                                                                                                                                                                                                                                                                                                                                                                                              G.
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                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowe
                                                                                                                                                                                                                                                                                                                                                                                                                                0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 80
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                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Unidentified

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ARBSULT 12
AAD32907/c
ID AAD329
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AAD329
XX
AC AAD329
XX
AC Plasmi
XX
DE Plasmi
XX
Diverg
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                                                                                                                                                                                                                                                                                                                                                                                                            proteins and polynucleotides encoding such proteins. The nucleic acid consequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rateliately, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is 1X ELVISILVES complementary repeat region DNA found in plasmids pKS106 and pKS124. This sequence is used in the exemplification of the invention of for the suppression of Fad2 in soybean
                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                      AAD32907 standard; DNA; 80
 Diverged delta-9
                              Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
                                                                01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly - and unsaturated fatty acids and in increasing the unsaturation levels
                                                                                              AAD32907;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 43; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DUPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2000; 2000US-0226996P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2001; 2001WO-US026246
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                                                                                                                                                                                                    61
                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                            38
                                                                                                                                                                                                                                                                                                                            ; 08
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                    GAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                                                                         CGGCCGGAGCTGGTCATCGTCGAGTCGGCGGCCGACTCGACGATGAGC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                        ₿P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to diverged delta-9 fatty acid desaturase d polynucleotides encoding such proteins. The nucleic acid
                                                                                                                                                                                                                                                                                                                           Conservative
                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                      12 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
fatty acid desaturase; enzyme; cellular lipid; oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (45. .74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "ELVISLIVES protein"
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                                                                                                                                                                                                                                                                                                                    51.9%; 50.
100.0%; Pr
                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                      28 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hitz WD,
                                                                                                                                                                                                                                                                                                                                        Score 80; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    28 G; 12 T; 0 U; 0
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                                                                                                                                                                                                                                                                                                                           Pred. No. 2. 
; Mismatches
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                                                                                                                                                                                                                                                                                                                         2.2e-10;
hes 0;
                                                                                                                                                                                                                                                                                                                                                         DB 6;
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                                                                                                                                                                                                                                                                                                                                                    Length 80;
                                                                                                                                                                                                                                                                                                                                                                                    Other;
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ABK1071
ID AB
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AC AB
XX

ABK10712 standard;

DNA;

92 ВP

ABK10712

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The present invention relates to diverged delta-9 fatty acid desaturase corrections and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular clipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polymeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFIP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106 and pKS124. This sequence is nearly in action in exemplification of the invention
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly and unsaturated fatty acids and in increasing the unsaturation levels in cellular lipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Page 43; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plant; gene mapping; immunisation; plasmid pKS124; plasmid pKS106; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2000; 2000US-0226996P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                       the suppression of Fad2 in soybean
                                                                              80
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8
                                                                                                                                                                                              ; 0B
                                                                                                                                                                                                                            Similarity
GAGATGACCAGCTCCGGCCG
                                                                                                                  CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
                                                                                                                                                                                                                                                                                                              08
                                                                              CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cahoon RE,
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                              BP; 12 A; 28 C; 28 G; 12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ELVISLIVES complement(45...74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "ELVISLIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                               51.9%; Sur
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitz WD,
                                                                                                                                                                                           Score 80; DB; pred. No. 2.20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinney AJ,
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                                                                                                                                                                                                                      DB 6; Le
2.2e-10;
                                                                                                                                                                                                                                                                                                           0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yadav NS
                                                                                                                                                                                           ٥,
                                                                                                                                                                                                                                                    Length 80
                                                                                                                                                                                           Indels
                                                                                                                                                                                           0,
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05-JUN-2002

(first

entry)

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RESULT 14
ABK10712/c
ID ABK10712 standard; DNA; 92 B
XX
AC ABK10712;
XX
DT 05-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                 문
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to plastidic phosphoglucomutase polypeptides and CC their related nucleic acids. The sequences are useful for producing a CC transgenic plant, by transforming a plant cell with a polymucleotide of CC the invention and regenerating a plant from the transformed plant cell. CC Polymucleotide fragments are useful for suppressing the level of CC expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polymucleotide that affects the CC level of expression of a plastidic phosphoglucomutase polypeptide in a CC least 541 nucleotides, measuring the level of the polypeptide in the CC plant cell containing the polymucleotide, and comparing the level of the polypeptide in the CC plant cell containing the polymucleotide, and comparing the level of the containing the polymucleotide with the cell containing the polypeptide in a plant cell that does not contain the CC the level of the polypeptide in a plant cell that does not contain the cliscated polymucleotide. A method for altering the level of expression of CC a plastidic phosphoglucomutase protein in a host cell comprises CC cell under conditions that are suitable for expression of the chimeric CC gene, where the expression of the gene results in production of altered CC levels of plastidic phosphoglucomutase. This sequence represents an CC invention
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                                                                                                                                                                                                             Sequence 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-156692/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-2000; 2000US-0218712P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plastidic phosphoglucomutase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artificial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                levels.
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                                                                                                                                                 67
                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                8O;
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Page 19; 27pp; English
                                                                                                                                                                     GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                   CGGCCGGAGCTGGTCATCTCGCCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
                                                                                                                                                 GAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                             16 A;
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                                                                                                                                                                                                                                                                                             51.9%;
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                                                                                                                                                                                                                                                                                                                                               <u>ن</u>
                                                                 ВP
                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                             Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                               30 G; 16 T;
                                                                                                                                               98
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                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ilag LL;
                                                                                                                                                                                                                                                                                             DB 6; Le
2.2e-10;
                                                                                                                                                                                                                                                                                                                                               0 U; 0 Other;
                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                             Length 92;
                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                Gaps
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RESULT 15
AAD29232
ID AAD29
XX
AC AAD29
XX
AC AAD29
XX
XX
DT 07-MA

AAD29232;

AAD29232 standard;

DNA;

92

26

GAGATGACCAGCTCCGGCCG 7

07-MAY-2002

(first entry)

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                                                                                                                                                                               The invention relates to plastidic phosphoglucomutase polypeptides and CC their related nucleic acids. The sequences are useful for producing a CC transgenic plant, by transforming a plant cell with a polynucleotide of CC the invention and regenerating a plant from the transformed plant cell. CC pólynucleotide fragments are useful for suppressing the level of CC expression of a gene encoding a polypeptide having plastidic CC phosphoglucomutase activity. An isolated polynucleotide that affects the CC level of expression of a plastidic phosphoglucomutase polypeptide in a CC level of expression of a plastidic phosphoglucomutase polypeptide in the plant cell can be identified by introducing a DNA fragment comprising at CC least 541 nucleotides, measuring the level of the polypeptide in the polypeptide in the polypeptide, and comparing the level of the polypeptide in the polypeptide in the plant cell containing the isolated polynucleotide with CC the level of the polypeptide in a plant cell that does not contain the CC isolated polynucleotide. A method for altering the level of expression of cell under conditions that are suitable for expression of the transformed CC cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered contained in the plastidic phosphoglucomutase. This sequence represents an of the chimeric particle.
                                                                                                        Query Match
Best Local S
Matches 80
                                                                                                                                                                             Sequence 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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                                      86
   98
                                                                       38
                                                                                                         l Similarity
80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Page 19; 27pp; English.
   GAGATGACCAGCTCCGGCCG 117
                                      CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
                                                                     Butler KH,
                                                                                                                                                                             BP;
                                                                                                           Conservative
                                                                                                                                                                               16
                                                                                                  51.9%; sc.
/ 100.0%; Pr
                                                                                                                                                                             A; 30 C; 30
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                                                                                                        Score 80; DB; Pred. No. 2.2
                                                                                                                                                                             G; 16 T;
                                                                                                  DB 6; Lc.
3. 2.2e-10;
0;
                                                                                                                                                                             0 U; 0
                                                                                                                                          Length
                                                                                                                                                                               Other;
                                                                                                           Indels
                                                                                                                                            92
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                                                                                                         Gaps
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RESULT 16
AAD29232/c
ID AAD292
XX
AC AAD292
XY
DT 07-MAY
XX
ELVISL
XX
KW Recomb
XX
OS
Uniden
XX
WO2002
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is a PCR primer used for amplifying ELVISLIVES complementary region DNA used in the exemplification of the invention
 WO200200904-A2
                                                    Recombinant construct;
                                                                              ELVISLIVES complementary region DNA amplifying PCR primer
                            Unidentified
                                                                                                                 07-MAY-2002
                                                                                                                                             AAD29232;
                                                                                                                                                                       AAD29232 standard; DNA; 92
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 37; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-139927/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-2000; 2000US-0213961P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant construct; gene expression; PCR primer;
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PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                      GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                               GAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 16 A; 30 C;
                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                 51.9%; bred. No.
100.0%; Pred. No.
'ive 0; Mismatches
                                                                                                               entry)
                                                   gene expression; PCR primer; ss
                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                  30 G; 16 T; 0 U; 0 Other;
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                      Length 92;
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RESULT 17
ABK10710
ID ABK10
XX ABK10
XX OS-JU
DT 05-JU
DX Artif
XX Plast
XX Plast
XX Plast
XX PLSS
FT CDS
FT CDS
FT CDS
FT X EP117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to mucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is a PCR primer used for amplifying ELVISLIVES complementary region DNA used in the exemplification of the invention
EP1174510-A2
                                                                                                                            Synthetic.
                                                                                                                                                      Plastidic phosphoglucomutase; transgenic; plant; gene; ds
                                                                                                                                                                                       Artificial
                                                                                                                                                                                                                  05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                             ABK10710
                                                                                                                                                                                                                                                                         ABK10710 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 37; 77pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nichols
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                                                                                                                                                                                                                                                                                                                                                                                                    CGGCCGGAGCTCGTCATCGCTCATCGTCGAGTCGGCCGCCGACTCGACGATGAGC
                                                                                                                                                                                    DNA sequence #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%; So illarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B₽;
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                         /*tag= a
/product= "ELVISLIVES peptide"
/partial
/note= "No start or stop codon
                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 30 C;
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                        start or stop codon shown"
                                                                                                                                                                                                                                                                         ВP
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G; 16 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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ABK10710/c
ID ABK107
XX
AC ABK107
AC ABK107
AC AFTIfi
XX
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Plasti
XX
Synthe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC Polynucleotide fragments are useful for suppressing the level of CC expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the CC level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at CC least 541 nucleotides, measuring the level of the polypeptide in the CC plant cell containing the polynucleotide, and comparing the level of the polypeptide in the CC plant cell containing the polynucleotide, and comparing the level of the cC polypeptide in the polypeptide in a plant cell that does not contain the CC the level of the polypeptide in a plant cell that does not contain the CC the level of phosphoglucomutase protein in a host cell comprises CC a plastidic phosphoglucomutase protein in a host cell comprises CC cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered CC levels of plastidic phosphoglucomutase. This sequence represents an CC artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the contract of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                 Artificial
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                                                                                                                                                                                                                          Plastidic phosphoglucomutase; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                               ABK10710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                 sequence #2.
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     /product= "BLVISLIVES peptide"
/partial
                                                                                                                Location/Qualifiers
                                                   /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 G;
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 T; 0 U; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
0.12;
                                                                                                                                                                                                                          plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 19
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ID AAC89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to plastidic phosphoglucomutase polypeptides and CC their related nucleic acids. The sequences are useful for producing a CC transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. CC polynucleotide fragments are useful for suppressing the level of CC expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the CC level of expression of a plastidic phosphoglucomutase polypeptide in a CC level of expression of a plastidic phosphoglucomutase polypeptide in the plant cell can be identified by introducing a DNA fragment comprising at CC plant cell containing the polynucleotide, and comparing the level of the polypeptide in the plant cell containing the isolated polynucleotide with CC the level of the polypeptide in a plant cell that does not contain the CC polypeptide in the plant cell containing the isolated polynucleotide with CC the level of the polypeptide in a plant cell that does not contain the CC isolated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises CC transforming a host cell with a chimeric gene and growing the transformed CC cell under conditions that are suitable for expression of the chimeric gene and growing the chimeric containing the production of altered levels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                       alpha 1I subunit; epilepsy; drug screening;
                                                                                                                              Human brain T calcium channel alpha 1G
                                                                                                                                                                     07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Page 19; 27pp; English.
                                   Homo sapiens.
                                                                                                                                                                                                                                              AAC89216 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-2001; 2001EP-00306143
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                                                                                          channel; human; brain T calcium channel; alpha 1G subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-156692/21.
DB; AAU77109.
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                                                                                                                                                                                                                                                                                                                                                                               74 GCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlson TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 6;
Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                            subunit gene exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                 117
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WO200070044-A2

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RESULT 20
AAC89216;
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XX AAC89216;
XX DE Human bra:
XX Ion channe
XX Ion cha
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Best Local S
Matches 51
                                                                                                  13-MAY-1999;
04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences for the human brain T calcium channel alpha 1G and alpha 1I subunits. The alpha 1G subunit gene (designated CACNAIG) consists of 38 exons, and alternative processing leads to the production of 64 different proteins. The alpha 1I subunit (designated CACNAII) consists of 37 exons, and 8 proteins are produced due to alternative processing. The sequences provided by the invention are useful for screening drugs for use in the
                                                                                                                                                                       08-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                       Ion channel, human, brain T calcium channel, alpha alpha 1I subunit; epilepsy; drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2001
                                                 (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                            WO200070044-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 19; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Splice variants of the human brain T calcium channel alpha 1G and alpha 1I subunits and genes encoding the subunits, useful as targets for antiepileptic drugs or for testing compounds or compositions useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGAGCTGCGGAAGAGCCTGCTGCCGCCTCTCATCATCCACACGGCCGCCACACCCATGT
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nilarity 58.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               T calcium channel alpha 1G subunit gene exon 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agnew WS;
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                                                                                               99US-0134063P.
99US-0137547P.
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99US-0137547P.
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Pred. No. 4.2e
0; Mismatches
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RESULT 21
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding program; inheritance; desired characteristic; growth; development; disease resistance; environmental adaptability; quality; yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023; structural gene; functional gene; regulatory gene; corn ear-specific profile; gene transcription; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences for the human brain T calcium channel alpha 1G and alpha 1I subunits. The alpha 1G subunit gene (designated CACNA1G) consists of 38 exons, and alternative processing leads to the production of 64 different proteins. The alpha 1I subunit (designated CACNA1I) consists of 37 exons, and 8 proteins are produced due to alternative processing. The sequences provided by the invention are useful for screening drugs for use in the
                                                                                                                                                                                                                                                                                                              26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corn ear-derived polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999;
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                                                                                                                                                                                                                                                         (INCY-) INCYTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 BP;
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                                                                                                                                                                                                                                                         GENOMICS INC
                                                                                                                                                                                                                                                                                                                 98US-0086722P
                                                                                                                                                                                                                                                                                                                                                                  99US-00313294
                                                                                                                                                                                               ĻΥ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 A; 72 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29.4;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (cpd) #6653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ţ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            贸
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
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development evaluating,

purified corn-ear derived polynucleotide useful as hybridization for detecting polynucleotide in sample, and for identifying, atting, and altering desired characteristics associated with growt

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RESULT 22
ABX88193/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 64
                                                                                                                                                                                                  Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SA structural gene; functional gene; regulatory gene; corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding program; inheritance; desired characteristic; growth; development; disease resistance; environmental adaptability; quality; yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cpds are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn ear-derived polynucleotides (cpds) of the invention. Note: The sequence data for this part and not form part of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022 and SATMON023. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development disease aresistance environmental adaptability.
                     14-MAY-1999;
                                                                                                                                                                                  multigene
                                                                                                                                                                                                                                                                                                                                                  Corn ear-derived polynucleotide (cpd) #6653
                                                            05-NOV-2002.
                                                                                                     US6476212-B1
                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX88193 standard; cDNA; 197 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; SEQ ID NO 6653; 390pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AGTCAGGAGCAAGATGGGTGCCGGCGGCAGGATGACCGAGAAGGAGCGGGAGAAGCAGGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccecc 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGATGAGCGAGATGACCAGCTCCGGCCGACCTCGACGATGAGCGAGATGACCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGCGGTGTCCGCCCGATCTGCTCTGCCCCGACGCAGCTGTTACNTCCTCCTCAGTCTC
                                                                                                                                                                                  trait;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 42
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                     9908-00313294
                                                                                                                                                                                  plant; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 55 C; 68 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.2%;
51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB
Pred. No. 9.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                         SATMON022; SATMON023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
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RESULT 23
AAL44709
ID AAL447
XX AAL44
XX AAL44
XX O3-MA
DT O3-MA
XX Human
XX Human
XX Human
XX neurc
KW Alzhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc useful for detecting cpds in a sample, for producing a corn ear-specific cc profile of gene transcription, for detecting altered gene expression in cc inbred or hybrid plants, and for screening several molecules for specific binding to the polynuclectide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA cc libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breading cc programs. Preferably, the cdps are used to identify, evaluate, alter, or cf follow the inheritance of desired characteristics associated with growth can development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful as molecular markers for cstudying inheritance and multigene traits in a plant breeding program. The cpds are useful for producing urrified corn-ear polypeptides by crecombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX99140 represent corn ear-derived copolynuclectides (cpds) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained corn electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                    neurodegenerative disorder; Huntington's disease; Parkinson's disease;
Alzheimer's disease; schizophrenia; mood disorder; dementia;
                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and SATMON023. Some of the cpds uniquely identify structural, fu
and regulatory genes of corn ear. The polynucleotides sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with growth,
                                                                                                Human glutamate receptor delta-1 subunit coding sequence
                                                                                                                                        03-MAY-2002
                                                                                                                                                                                                                    AAL44709 standard; DNA; 156 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; SEQ ID NO 6653; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal
                                                                                                                                                                                                                                                                                                                                                         123 TCGAC 127
                                                                                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                    67 GCGCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                         glutamate receptor delta-1 subunit; epilepsy; brain damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                GCTGCTCCTGCTTCTCCCGCTCCTTCTCGGTCATCCTGCCGCCGGCACCCATCTTGCTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to the isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B₽;
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0086722P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (cdps)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Y.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 A; 55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.2%;
51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the corn (Zea mays)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 G; 30 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       묫
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of corn ear-derived cDNA libraries SATMON022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 197,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ear-derived
                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                  IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            functional,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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anticonvulsant;

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RESULT 24
AAL44709/c
ID AAL447
XX AAL447
AC AAL447
AC AAL447
XX Human
DE Human;
KW Human;
KW neurod
KW neurod
KW neurop
KW neurop
KW uropat
XX
XX
BOS Homo s
XX
PD 24-JAN
XX
                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                       Š
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                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a human glutamate receptor delta-1 subunit polypeptide. This can be used to screen for agents which modulate the activity of glutamate receptor delta-1 subunit polypeptide, which may then be used in the treatment of diseases such as epilepsy, brain damage, neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, and Parkinson's disease, schizophrenia, mood disorders, pain, neuropathologic pain and dementias. The present sequence is a fragment of the human glutamate receptor delta-1 subunit coding sequence
                                                                                                                         Human; glutamate receptor delta-1 subunit; epilepsy; brain damage; neurodegenerative disorder; Huntington's disease; Parkinson's disease; Alzheimer's disease; schizophrenia; mood disorder; dementia;
                                                                                                 neuroprotective; vasotropic;
                                                                                                             neuropathological pain; pain; receptor; anticonvulsant; nootropic;
                                                                                                                                                                                                                                                    AAL44709 standard; DNA; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human glutamate receptor delta-1 subunit protein which can be regulated for treating epilepsy, schizophrenia, neurodegenerative diseases, ischemia, pain, benign prostate hyperplasia and urinary
                                       WO200206313-A2
                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kossida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUL-2001; 2001WO-EP008102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic; uropathic; antiparkinsonian; vulnerary; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                incontinence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-195800/25
                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                        GACTCGACGATGA 132
                                                                                                                                                                                                                                                                                                                GCCTCAACGATGA 80
                                                                                                                                                                                                                                                                                                                                                                                       TCATCGTCGAGTCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCC 119
                                                                                                                                                                                                                                                                                                                                                                   TCTTCGAGGAGAACGCGGCCAAGGACGACAGGTTTCCAGTTGGCGGTATCCGACCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 9;
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0218835P
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                         receptor delta-1 subunit coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 45 C; 44 G;
                                                                                                                                                                                                                                                                                                                                                                                                                             17.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                     ₽₽
                                                                                                 analgesic; neuroleptic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 26.6; DB
Pred. No. 2e+03;
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                            ID NO:
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Matches
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Best Local
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                                                                                                                                                                                                     WO200206313-A2
                                                                                                                                                                                                                                                                                                                neurodegenerative disorder; Huntington's disease; Parkinson' Alzheimer's disease; schizophrenia; mood disorder; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL44706
                                                                                                     18-JUL-2000;
                                                                                                                                    13-JUL-2001; 2001WO-EP008102
                                                                                                                                                                      24-JAN-2002
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                   neuroprotective; vasotropic;
                                                                                                                                                                                                                                                                                                  neuropathological
                                                                                                                                                                                                                                                                                                                                                  Human; glutamate receptor delta-1 subunit; epilepsy; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human glutamate receptor delta-1 subunit protein which can regulated for treating epilepsy, schizophrenia, neurodegenerative diseases, ischemia, pain, benign prostate hyperplasia and urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Fig 9; 97pp; English.
                                                                       (FARB )
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                                                                                                                                                                                                                                                                                                                                                                               glutamate receptor delta-1 subunit coding sequence
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                                                                       BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTCCTCGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTCGACGATGA 95
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                                                                                                     2000US-0218835P
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                       ĀG
                                                                                                                                                                                                                                                                  pain; pain; receptor;
vasotropic; analgesic;
rkinsonian; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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60.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26.6; DB
Pred. No. 2e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 T; 0 U; 0
                                                                                                                                                                                                                                                                   neuroleptic; cytostatic;
gene; ds.
                                                                                                                                                                                                                                                                                                    anticonvulsant;
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                                                                                                                                                                                                                                                                                                                                 Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                                                   damage;
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                                                                                                                                                                                                                                                                                                                                  disease;
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RESULT 26
AL44706/c
ID AL447
XX AL447
XX AL447
XX ALM447
XX ALM447
XX Human;
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                                                                                                                                             Novel human glutamate receptor delta-1 subunit protein which can be regulated for treating epilepsy, schizophrenia, neurodegenerative diseases, ischemia, pain, benign prostate hyperplasia and urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human glutamate receptor delta-1 subunit protein which can be regulated for treating epilepsy, schizophrenia, neurodegenerative diseases, ischemia, pain, benign prostate hyperplasia and urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disorder; Huntington's disease; Parkinson's disease, Alzheimer's disease; schizophrenia; mood disorder; dementia; neuropathological pain; pain; receptor; anticonvulsant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uropathic; antiparkinsonian; vulnerary; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 97pp; English.
                                                                                                                                                                                                                                                                     WPI; 2002-195800/25
                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2000; 2000US-0218835P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-2001; 2001WO-EP008102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200206313-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; vasotropic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL44706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL44706 standard; DNA; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 190
                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTCGACGATGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTCAACGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTCGAGGAGAACGCGGCCAAGGACGACAGGGTGTTCCAGTTGGCGGTATCCGACCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 45 A; 57 C; 53 G; 35 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         8
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delta-1 subunit coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26.6;
Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
. 2e+03;
. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroleptic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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The present invention

provides a human glutamate receptor delta-1 subunit

Disclosure;

Fig 2; 97pp;

English.

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RESULT 27
RAC09904
ID AAC09
XX AC09
XX DE Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Homo
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                 mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide. This can be used to screen for agents which modulate the activity of glutamate receptor delta-1 subunit polypeptide, which may then be used in the treatment of diseases such as epilepsy, brain damag neurodegenerative disorders such as Alzheimer's disease, Huntington's disease and Parkinson's disease, schizophrenia, mood disorders, pain, neuropathologic pain and dementias. The present sequence is a fragment the human district and communities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC09904 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 190 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AÁC09904;
                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 13979; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2000; 2000EP-00200610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5' EST; expressed sequence tag; secreted protein; cDNA isolation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATCGTTGAGGCTCAGGTCGGATACCGCCAACTGGAACACCCTGTCGTCCTTGGCCGCG 33
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nilarity 60.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edwards J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO: 13979
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AAC09904/c
ID AAC09904 standard; cDNA; 195
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Best Local
                                                                                                              The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted protesins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                          Sequence 195
                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST;
gene therapy;
                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards
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                                                     Similarity
CGAGTCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGA
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                                          Conservative
                                                                                                                                                                                                                                                                                                                            forensic,
                                                                                                                                                                                                                                                                                                ID NO 13979; 71pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                           gene therapy and chromosome mapping
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                                                                                        58 G; 32 T;
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RESULT 30 AAL17387/ ID AAL1

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RESULT 29
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0219115P.
09-JUN-2000; 2000US-0219115P.
25-JUL-2000; 2000US-0220534P.
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human breast cancer expressed polynucleotides (AALO'544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                Sequence 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1753; 3695pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide useful as a marker for the diagnosis
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50; Conserv
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  GCTCGTCGATCACCGACACTTCCAGGTCGG
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Pred. No.
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Best Local
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14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
                                                                                                                                                                                                                                                                               Sequence 170
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 Homo sapiens.
                    Human; breast cancer; cell marker; cytostatic; ss
                                        Human breast
                                                              07-DEC-2001
                                                                                  AAL09498;
                                                                                                     AAL09498 standard; cDNA; 189
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1753; 3695pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lillie J,
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09-JUN-2000;
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2000US-0192099P.
2000US-0193480P.
2000US-0205230P.
2000US-0211315P.
                                                                                                                                                                                                                                       Conservative
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                                        polymucleotide
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RESULT 32
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Best:Local :
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14-MAR-2000;
24-MAR-2000;
14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
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15-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 189
                                                                                                                                Homo sapiens.
                                                                                                                                                          Human;
                                                                                                                                                                                   Human breast cancer expressed polynucleotide 1955.
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                                                                                                                                                                                                                                                                AAL09498
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                                                                                                                                                          breast
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; 2000US-0176077P.
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                                                                                                                                                          cell marker; cytostatic; ss
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Pred. No. 2.8e+03;
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RESULT 33
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                                                                       WPI; 1997-034393/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filamentous; fungus; Byssochlamys nivea; Neosartorya fischeri; primer; Zygosaccharomyces bailii; PCR; amplification; polymerase chain reaction; ribosomal internal transcribed spacer; detection; heat resistant; fruit;
                                                                                                                                                                                                                                                                  31-MAY-1996;
                                                                                                                                                                                                                                                                                                                 05-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                        Neosartorya fischeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                       microorganism;
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15-MAY-2000; 2000US-0205230P.
09-UUN-2000; 2000US-0211315P.
25-UUL-2000; 2000US-0220534P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       contaminant; strawberry;
                                                                                                                                                                                                                95FR-00006578
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55.6%;
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No.
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Primers derived from

contaminants

n internal transcribed spacer sequences of foodstuffs, esp Byssochlamys nivea,

Neosartorya

used

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RESULT 34
ANT49353/c
ID ANT493
XX ANT493
XX ANT493
XX IO-SEP
XX Filame
XW Eygosa
XW Filame
XW MO9638
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Best Local
       The invention relates to methods to detect the filamentous runy. Byssochlamys nivea, Neosartorya fischeri and Zygosaccharomyces bailii PCR amplification on genomic DNA using primers derived from the ribosc internal transcribed spacer (ITS) sequences (see AAT49351-6). This sequence represents the ITS1 from N. neosartorya and is amplified by primers AAT49359-60. The method is used to detect heat resistant primers AAT49359-60 because which are important contaminants
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-034393/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neosartorya fischeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Filamentous; fungus; Byssochlamys nivea; Neosartorya fischeri; primer; Zygosaccharomyces bailil; PCR; amplification; polymerase chain reaction; ribosomal internal transcribed spacer; detection; heat resistant; fruit; microorganism; contaminant; strawberry; foodstuff; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N. fischeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to methods to detect the filamentous fungi Byssochlamys nivea, Neosarcorya fischeri and Zygosaccharomyces bailii PCR amplification on genomic DNA using primers derived from the ribos internal transcribed spacer (ITS) sequences (see AAT49351-6). This sequence represents the ITS1 from N. neosartorya and is amplified by primers AAT49359-60. The method is used to detect heat resistant microorganisms of the above species which are important contaminants fruit, especially strawberry-based foodstuffs
                                                                                                                                                                                                                                                                                 fischeri or
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chrzavzez E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1995;
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                                                                                                                                                                                                                                                                                                           contaminants
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                                                                                                                                                                                                                                                                                                    derived from internal transcribed spacer sequences contaminants of foodstuffs, esp Byssochlamys nivea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIR
                                                                                                                                                                                                                                Page 12; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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59.7%;
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Pred. No. 3.
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    used to
    Neosartorya

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                                                                       The present sequence was used in a method for generating RNA-protein CC fusions, which comprise a protein covalently linked to the 3' end of its cown mRNA. The fusions are made by synthesis and in vitro or in situ translation of an mRNA molecule with a peptide acceptor attached to its C3' end. The RNA-protein fusions are incubated under high salt conditions cto produce a protein library. This method is useful for improving or CC altering existing proteins, as well as for isolating new proteins and cnucleic acid or small molecule targets. It may also be used to improve human or humanised single-chain antibodies for the treatment of a number of diseases. The method is useful for the isolation of proteins with genes on the basis of protein, for screening cDNA libraries and cloning new genes on the basis of protein interactions. Unlike prior art, the new method does not rely on maintaining the integrity of an enthod seems the protein and the nucleic acid so that the information of the between the protein and the nucleic acid so that the information of the protein is retained and can be recovered in readable, nucleic acid form
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                             Producing protein or DNA libraries which are useful for improving existing proteins, by in vitro translating protein coding sequences to produce RNA-protein fusions and incubating these protein fusions under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 183 BP; 30 A; 62 C;
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                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberts RW,
                                              BP; 4 A; 15 C; 8 G; 15 T; 0 U; 81 Other;
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16.2%;
15.0%;
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Score 25;
Pred. No.
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Query Match Best Local Similarity

DB 3;

밁 δ

118

GAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACCTCGAC Local

Similarity

16.2**%**; 15.0**%**;

Conservative

26;

Score 25; DB 3; Pred. No. 4.8e+03; 6; Mismatches 65

65:

0

Gaps

0

Length 123 Indels

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RESULT 36
AAA94339/c
ID AAA943
XX
AC AAA943
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                          altering existing proteins, as well as for isolating new proteins and nucleic acid or small molecule targets. It may also be used to improve human or humanised single-chain antibodies for the treatment of a number of diseases. The method is useful for the isolation of proteins with specific binding properties, for screening cDNA libraries and cloning new genes on the basis of protein-protein interactions. Unlike prior art, the new method does not rely on maintaining the integrity of an mRNA:ribosome:nascent chain ternary complex, which is very fragile and is therefore of limited use. The method does not rely on topological links between the protein and the nucleic acid so that the information of the protein is retained and can be recovered in readable, nucleic acid form
Sequence 123 BP; 4 A; 15 C; 8 G; 15
                                                                                                                                                                                                                    translation of an mRNA molecule with a peptide acceptor attached to its 3' end. The RNA-protein fusions are incubated under high salt conditions to produce a protein library. This method is useful for improving or
                                                                                                                                                                                                                                                                          The present sequence was used in a method for generating RNA-protein fusions, which comprise a protein covalently linked to the 3' end of own mRNA. The fusions are made by synthesis and in vitro or in situ
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 72; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Producing protein or DNA libraries which are useful for improving existing proteins, by in vitro translating protein coding sequences to produce RNA-protein fusions and incubating these protein fusions under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA94339,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Szostak JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-protein fusion; protein library; protein isolation; gene cloning;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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T; 0 U; 81 Other;
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                                                                                                                                                                                                                                                                                                            RNA-protein
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RESULT 37
ACH88658
ID ACH88658
XX ACH88
XX Human
XX Human
XX Human
XX Homo
CC expression, comprising any of the 27,400 fully defined nucleotide CC sequences in the specification, or their complements or fragments, and CC encoding at least 8 amino acids of any of the 6888 amino acid sequences CC fully defined in the specification. The probe is a single exon probe that CC hybridises under high stringency conditions to a nucleic acid molecule CC expressed in human cells or tissues. Also included are a spatially-CC addressable set of single exon nucleic acid probes for measuring human CC gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately CC and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of CC probe cited above, an ORP-encoded peptide comprising at least 8 CC contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid substitutions), an CC contiguous amino acids of any of the above- mentioned amino acid substitutions), an CC contiguous amino acids specifically to appetide cited above, or solated antibody that binds specifically to appetide cited above, or solated antibody that binds specifically to appetide cited above, or solated antibody that binds specifically to appetide contain the expression and appearance of providing contains a database having a plurality of records contain second second contains a database having a plurality of records contain their specifically to appear the single exon microarrays. In addition, the probes are used in identifying and chara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human genome-derived single exon nucleic acid probes useful for gene expression analysis, for identifying or characterizing alternatesplicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 21853; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-119264/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome derived single exon probe #21853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PENN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENN S G.
RANK D R.
HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNNSNNSNNSNNSNNSNNSNNSNNSNNSGÅTGCACAÅG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above,

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe the hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human reasons according to the second second probes for measuring human reasons.

that

New human genome-derived single exon nucleic acid probes useful for gene expression analysis, for identifying or characterizing alternat splicing events, for assessing genomic alterations or as tools for

alternative

human

Claim 1; SEQ ID NO 21853; 80pp; English

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RESULT 38
ACH88658/c
ID ACH8866
XX ACH8866
XX ACH8866
XX Human
XX Human;
XW Human;
XW altern
XX Homo 8
PN US2003
XX IFANX;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a hums single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome derived single exon probe #21853
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) RANK D R.
) HANZEL D K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTCCTGCCGCCTCGCCTCGGAGCCGGGAGACCAGCTTC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR,
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
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RESULT 39
ACD96616
ID ACD966XX
ACD96
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-colerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmod
                                                                                                                                                                                 Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of
                                                                                                                                                                                                                                                                                                                                           WPI; 2003-182626/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SIMP/) SIMPSON A J G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002155438-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer cell expressed cDNA #5028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACD96616 standard; cDNA; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRENTANI R R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frame detection; genome sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 15 A; 39 C; 34 G;
                                                                                                                                                                                                                                                                                                                                                                                                                  Neto ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00196716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00406117
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72.7%;
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Pred. No. 5.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trypanosome; Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                             primer at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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The invention describes a method of determining open reading frames

27-SEP-1999;

9905-00406117

24-OCT-2002.

Example 9; Page 721; 959pp; English

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RESULT 40
ACD96616/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC nucleotide sequence from a genome of an organism corresponds to a contile sequence of an open reading frame; for preparing a contig, concleic acid molecule from a genome of an organism; and for sequencing call or part of a genome of an organism. mRNA is obtained from mammalian cor human cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of colon cancer or breast cancer cell. The method is useful for analyses of colon cancer or breast cancer cell. The method is useful for analyses of colon cancer or breast cancer cell. The method is useful for analyses of colon cancer or breast cancer cell. The method is useful for analyses of colon cancer and so forth. The method can be used to study living cystems to determine if, e.g. there have been genetic shifts which render can individual or population more or less likely to be afflicted with congenital diseases, and the risk of affliction to a feetus, as well as the study of whether the conditions are likely to be passed to offspring chrough ova or sperm. The analyses for pathological conditions can be carried out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be studied to determine if resistance genes are present, defects in plant condergone shifts or mutations, which may require different approaches to crypanosomes, different types of plasmodium, etc. The method essentially climinates sequencing of non-coding portions. This sequence represents a colymnucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting nucleic acids. The method is useful for: determining that a known
                                                                                                                                                                                                                 breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-toleranc; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmod.
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                     Open reading frame detection; genome sequencing; colon cancer;
                                                                                                                                                                                                                                                                                                                                              Human colon cancer cell expressed cDNA #5028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACD96616 standard; cDNA; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 130 BP;
                                                                                                                                                                                                              agriculture; foo:
influenza virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 GAGCGAGATGACCAGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 TCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGACTCGACGAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTGAGCTGACCTGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 A; 44 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%;
57.9%;
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Pred. No. 5.4e+
0; Mismatches
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                                                                                                                                                                                                                   trypanosome; Plasmodium;
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RESULT 41
AAC12537
ID AAC12
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AC AAC12
XX
DT 06-00
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                                                                                                                                                                                                                                                                                                                                                                                                                             CC nuclectide sequence of an open reading frame; for preparing a contig.
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism; and for sequencing
CC all or part of a genome of an organism; and for sequencing
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC carried out in all animals, plants, birds, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC undergone shifts or mutations, which integrate into the genome, such as
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of plasmoddium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC colonicated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                Query Match
06-OCT-2000
                                       AAC12537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with a single oligonucleotide primer (I) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting nucleic acids. The method is useful for: determining that a known
                                                                           AAC12537 standard; cDNA; 181 BP
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence from a genome of an organism corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 721; 959pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining open reading frames of genome of an organism e.g. a suffering from cancer involves use of single oligonucleotide prisons tringency for preparing single-stranded cDNA from mRNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-182626/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simpson AJG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NETO E D.
BRENTANI R R.
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                  CCTCTGCCTTCGCCCA 26
                                                                                                                                                                                                           AGTCGGCGGCCGA
                                                                                                                                                                                                                                                                                    GCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCG 68
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neto ED,
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     describes a method of determining open reading frames in organism, comprising contacting mRNA from cell of organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00196716.
                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                            16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                  A; 44 C; 35 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                                                                           84
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                                                                                                                                                                                                                                                                                                                                            Score 24.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                        i.4e+03;
ies 32;
                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                              Length 130;
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RESULT 42
AAC12537/c
ID AAC125
XX AC125
XX AC125
XX DT 06-OCT
XX Human
XX Human;
XW Gene t
XX Homo s
XX EPN EP1033
XX D6-SEP
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included.
                                                                                                                                                                                         06-OCT-2000
                                                                                                                                                                                                                       AAC12537
                                                                                                                                                                                                                                                     AAC12537
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 181 BP; 35 A; 35 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                             Homo sapiens
                                                                                                                                                          Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                           5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' EST; expressed sequence tag; secreted protein; cDNA isolation;
herapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                        ATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCG
                                                                                                                                                                                                                                                   standard; cDNA; 181 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                   ATCCCCTACTCTGCGGGCGCGAGGCGTCTGGCTCTTCGCGGCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                       (first
                                                                                                         ; expressed sequence tag; chromosome mapping; ss.
                                                                                                                                                        protein 5' EST, SEQ ID NO: 16612.
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                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 G;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 T; 0 U; 0 Other;
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                                                                                                                           secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                       5.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 181;
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                                                                                                                           cDNA isolation;
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06-SEP-2000 EP1033401-A2

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ARESULT 43
ADS6952
ID ADS69
XX ADS69
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AC ADS69
XX 18-NC
COrn
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XX COrn;
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XX Z01-NI
XX 12-MJ
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PR 21-AI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal disease; bacterial infection; disease resistance infest in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn seedling-derived polynucleotide (cpds), SEQ ID 4668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 181 BP; 35 A; 35 C; 92 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      US2003237110-A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pollution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS69652 standard; cDNA; 164 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 16612; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2000; 2000EP-00200610
                                     (INCY-) INCYTE PHARM INC
                                                                                                12-MAY-1998;
21-APR-1999;
                                                                                                                                                                                                06-AUG-2001; 2001US-00923876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCGCCGCGAAGAGCCAGACGCCTCGCGCCGCCGCAGAGTAGGGGAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                              injury; pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                98US-0085331P.
99US-00298329.
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67.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24.8; DB 3;
Pred. No. 5.4e+03;
0; Mismatches 17;
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ADS6562/c
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                                                                                                                                                                                                                                                                                                                                                                             Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal disease; bacterial infection; Goss' Bacterial Wilt; blight; Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot; bacterial stripe; maize dwarf mosaic virus infection; environmental stress; water stress; pH stress; temperature stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corn seedling-derived polynucleotide (cpds), SEQ ID 4668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS69652 standard; cDNA; 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-195165/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCTC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ntion relates to a corn seedling-derived polynucleotide (cdp) from ADS64985-ADS71316, or their complements and fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGACTC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGACGACGATGCGGAAGCGGGATCTGGGCATCCTGCTGCTCGCCGCCTTCGCCATCTT 133
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                                                                                                                                                                                                                                                                                                                                      injury; pesticide.
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 164;
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06-AUG-2001; 2001US-00923876.

US2003237110-A9

25-DEC-2003

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RESULT 45
AAI27481
ID AAI27
XX AAI27
AC AAI27
XX 12-OC
XX 12-OC
XX Probe
XX Probe
XX Probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     included are a composition for the detection of altered expression of a code (comprising a polynucleotide selected from ADS64985-ADS71316), a method of detecting a polynucleotide in a biological sample using a cdp, camethod for using alignmers (and amplification) to recover a regulatory celement from a DNA library using oligomers designed against a cdp, a seedling specific regulatory element that regulates the expression of a cdp, an expression vector containing a cdp or regulatory element, a plant transformed with the vector, a host cell containing the vector (and cxpressing a compound which binds a CDP and screening a plurality of identifying a compound which binds a CDP and screening a plurality of compounds for binding to cdp polynucleotide. The cdp polynucleotides, contents, vectors, cells and antibodies are useful for the contents of contents, evaluation and alteration of seed growth and development, disease resistance (e.g. to insect infestation, fungal disease, bacterial for bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf useful carries infection) and resistance to environmental stress (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                  09-AUG-2001.
                                                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
cervical cancer; ss.
                                                     WO200157278-A2
                                                                                                                                                                          Probe #17414
                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                AAI27481;
                                                                                                                                                                                                                                                                                 AAI27481 standard; DNA; 185
                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 164 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    water stress, pH stress, temperature stress, pollution, pesticides. The present sequence is cdp cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4668; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New corn seedling-derived polynucleotides and polypeptides, useful in identifying and altering desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality
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21-APR-1999;
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                                                                                                                                                                       for gene expression analysis in human cervical cell sample
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99US-00298329.
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Pred. No. 6.7e+03;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                   Sequence 185 BP; 30 A; 65 C; 61 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 17414; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488901/53.
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2000US-0207456P.
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                                         Glassman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Low and Nichols, S.E.

Recombinant constructs and their use in reducing Patent: WO 0200904-A 13 03-JAN-2002;
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E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
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/mol_type="unassigned DNA"
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Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
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Recombinant constructs and their use in reducing gene expression Patent: WO 0.200904-A 12 03-JAN-2002;

E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
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Patent: WO 0216565-A 25 28-FEB-2002;
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/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="ELVISLIVES complementary
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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E. I. d
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Patent: WO 0216565-A 24 28-FEB-2002;
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Recombinant constructs and their use in reducing gene Patent: WO 0200904-A 12 03-JAN-2002;
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AX367127
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                                                                                                                                                         /organism="synthetic construct"
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/db_xref="taxon:32630"
/noTee="ELVISLIVES complementary
pKS124"
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/mol_type="unassigned DNA"
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AX392335/c
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DEFINITION
ACCESSION
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Patent: WO 0216565-A 24 28-FEB-2002;
E. I. du Pont de Nemours and Company
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Sequence 24 from
AX392335
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Sequence 14 from Patent W00200904.
AX367129
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E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
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/mol_type="unassigned DNA"
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/note="ELVISLIVES PCR prim
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30 CGAGTCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACCTCGA 89
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synthetic construct
other sequences; artificial sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glassman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.I. and Nichols, S.E. Recombinant constructs and their use in reducing gene expression Patent: WO 0200904-A 14 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14
AX367129
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                                         th 19.1%;
| Similarity 58.6%;
| S1; Conservative
                                                                                                                                                                       Mittman, S.T. and Agnew, W.S.
Human brain t calcium channel alpha-subunit
Patent: WO 0070044-A 16 23-NOV-2000;
The Johns Hopkins University (US)
                                                                                                                                                                                                                                                                                                                  AX047784
Sequence 16 from Patent
AX047784
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                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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/mol_type="unassigned DNA"
/mol type="unassigned DNA"
/db xref="taxon:32630"
/note="ELVISLIVES PCR primer"
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                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                         Score 29.4; DB 6;
Pred. No. 4.1e+04;
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Pred. No.
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                                                                                                                                                                                                                                                                                    Sequence 6653 from patent AR251294
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Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.
Polynuclectides and polypeptides derived
Patent: US 6476212-A 6653 05-MOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain t calcium channel alpha-subunit splice variants
Patent: WO 0070044-A 16 23-NOV-2000;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GACGATGAGCGAGATGACCAGCTCCGGCCGACTCGACGATGAGCGAGATGACCAGCT
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                                    GGCGCGGTGTCCGCCCGATCTGCTCTGCCCCGACGCAGCTGTTACNTCCTCCTCAGTCTC
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nilarity 51.2%;
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                                                                                                                                    /organism="unknown"
/mol_type="genomic
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Query Match
Best Local Similarity
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Aspergillus fumigatus
Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; Ascomycota; Mitosporic Trichocomaceae; Asperg
                                                                                                                                          Direct Submission
Submitted (18-APR-2003)
                                                                                                                                                                                                Detection and identification Unpublished
                                                                                                                                                                                                                                                                                                                                   Aspergillus fumigatus ITS1,
AJ557755
AJ557755.1 GI:46406330
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Lalgudi, R. V., Ito, L. Y. and Sherman, B. K.
Polynucleotides and polypeptides derived
Patent: US 6476212-A 6653 05-NOV-2002;
                                                                                                                              Universitaet Oldenburg,
                                                                                                                                                                                                                                                                                                                       internal transcribed spacer 1;
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/mol_type="genomic_DNA"
/isolate="8"
                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="genomic DNA"
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country="Germany:North
          specific_host="Alcyonidium"
db_xref="taxon:5085"
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Pred. No. 7.6e+04;
Pred. No. 7.6e+04;
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Strasse 9-11,
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                                                                RESULT 17
AX393064
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                               AX393064
Sequence 9
AX393064
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 Homo
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Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomy
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
                      AX393064.1
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-APR-2003)
Universitaet Oldenburg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus fumigatus ITS1,
AJ557755
                                                                                                                                                                                                                                                                                                                                                                                    GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Hain, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection and identification Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hain, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ557755.1 GI:46406330
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                                                                                                                                                        CGTTCATGTTGGGGTCTTCGGCGGGCGCGCGGGCGCGGGCGCAAGGCCTCCCCGGCGGCC
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sapiens
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1. .191
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1. .191
/note="internal transcribed spacer 1, ITS1"
                                          from
                                                                                                                                                                                                                                                                                         country="Germany:North
                                                                                                                                                                                                                                                                                                    specific host="Alcyonidium gelatinosum"
db_xref="taxon:5085"
                                                                                                                                                                                                                                                                                                                              isolate="8"
                                                                                                                                                                                                                                                                                                                                     organism="Aspergillus"
mol_type="genomic DNA"
                      GI:19701116
(human)
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61.1%;
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Pred. No. 1.1e.
0; Mismatches
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hes 28;
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AX393064/c
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Uncultured bacterium nirS isolate:DGGE band f2r5-ko.
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AX393064
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                                                                                                                                                                                                                                                                                                                                   Regulation of human glutamate receptor delta-1 subunit patent: WO 0206313-A 9 24-JAN-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
            AB164172.2
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Patent: WO 0206313-A 9 24-JAN-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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                                                                                                                         TTCTCCTCGAAGA 8
                                                                                                                                                  GACTCGACGATGA 95
                                                                                                                                                                                              TCATCGTTGAGGCTCAGGTCGGATACCGCCAACTGGAACACCCTGTCGTCCTTGGCCGCG
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                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DN/
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 bp
from Patent WO0206313.
            GI:45421893
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Primates;
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                                                                                                                                                                                                                       Score 26.6; DB 6;
Pred. No. 1.5e+05;
0; Mismatches 29;
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Pred. No. 1.5e+05;
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                                                                                                                                                                                                                                                           Uncultured bacterium nirS gene isolate: DGGE band f2r5-ko.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-FEB-2004) Tadashi Shoji, The University of To Department of Urban Engineering: 7-3-1, Hongo, Bunkyo, Toky 113-8656, Japan (E-mail:shoji@enrt) Tokyo.ac.jp, Tel:81-3-5841-7784, Fax:81-3-5841-8538)
On Mar 13, 2004 this sequence version replaced gi:45330784.
Submitted (26-FEB-2004) Tadashi Shoji,
                                                                                    Microbial communities of an enhanced biological phosphorus removal process using oxygen, nitrate and nitrite as electron acceptors
                                                                                                                                                                         uncultured bacterium uncultured bacterium
                                                                                                                                                                                                                                                                                               AB164172
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                 Direct Submission
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                                                                  process using oxygen,
Unpublished
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                                                    (bases 1 to 165)
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/transT_table=11
/producT="nitrite reductase"
/protein_id="BAD12410.2"
/protein_id="BAD12410.2"
/db_xref="GI:45421894"
/translation="YHPEPRVASIVASHFSPEFVVNVKETGKTLMVDYSNIDALKVTE
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|mol_type="genomic DNA"
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Pred. No. 1.4e+05;
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                                                                                                                                                                                                                                                                             for nitrite reductase, partial cds,
The University of Tokyo,
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                                                                                                                                                                                                       Regulation of human glutamate receptor delta-1 subunit Patent: WO 0206313-A 2 24-JAN-2002; Bayer Aktiengesellschaft (DE)
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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/country="Japan:Tokyo"
/note="PCR products amplified
nirS3R were analyzed by DGGE"
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/db_xref="GI:45421894"
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from Patent WO0206313.
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56.2%;
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Pred. No. 1.4e
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Pred. No. 1.4e+05;
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Sequence 2 from Patent WO0206313.
AX393057
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Bayer Aktiengesellschaft (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 13979 06-SEP-2000;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  CGAGATGACCAGCTCCGGCCGCCGACTCG 125
                           GCTGCGGCGGCRGTGTCTCGCGTTCGGCGGGATTTCTCTTCGCTCCGGCTCGGCCTAGGT 105
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llarity 60.3%;
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.4e+05;
0; Mismatches 29; Indels
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Pred. No. 1.4e+05;
0; Mismatches 39;
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Sequence 13979 1
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                                                                                                 C12N5/10,
PC C12P2
                                                                                                                                                                                                                                                           Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y. Sequence tag and encoded human protein Patent: JP 2001269182-A 9895 02-OCT-2001;
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195)
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                                                                                                                                                                                                                                                                                                                                                                                                                            BD033649
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                        Key
                                                                                                                            C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21,
                                                                                                                                                        JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                      24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
                                                                                               12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,
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/mol_type="unassigned DN
/db_xref="taxon:9606"
                                      Location/Qualifiers.
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/mol_type="genomic
  /organism="Homo sapiens"
/mol_type="genomic DNA"
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from Patent EP1033401.
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; Pred. No. 1.4e+
0; Mismatches
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1.4e+05;
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Best Local Similarity
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PN 0701269182-A/9895
PN 07-2001269182-A/9895
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10, C
                                                              AR427779
Sequence 19276
AR427779
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Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 9895 02-OCT-2001;
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Mammalia; Eutheria; Primates;
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JP 2001269182-A/9895.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Local Similarity 55.1%;
hes 49; Conservative
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Edwards,J.-B.D.M., Jobert,S. and Giordano, EST's and encoded human proteins

Patent: US 6639063-A 19276 28-OCT-2003;

Location/Qualifiers
Dumas Milne Edwards, J.B., Jobert, S. and ESTs and encoded human proteins Patent: EP 1104808-A 19276 06-JUN-2001;
                                                                                                                                                                                  Sequence 19276 from AX988473
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49; Conserv
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Edwards, J.-B.D.M., Jobert, S. and Giorda
EST's and encoded human proteins
Patent: US 6639063-A 19276 28-OCT-2003;
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                             Homo sapiens
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                                                                                                                                                                  AX988473.1 GI:40994650
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/mol_type="genomic DNA"
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/mol_type="genomic
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Pred. No. 1.7e+05;
1; Mismatches 39;
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Pred. No. 1.7e+05;
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RESULT 31
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Sequence 19276 from Patent EP1104808.
AX988473
GENSET CORP
         Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hom 1 (bases 1 to 171)
Edwards, J.B.D.M., Jobert, S. and Giordano, J.E. EST and encoded human protein
Patent: JP 2002010789-A 15409 15-JAN-2002;
                                                                                                                                                BD123332 171 b
EST and encoded human protein.
BD123332
                                                                                          Homo sapiens (human)
                                                                                                                     BD123332.1 GI:23218277
JP 2002010789-A/15409.
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Patent: EP 1104808-A 19276 06-JUN-2001;
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Mammalia; Eutheria; Primates;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.7e+05;
1; Mismatches 39;
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Pred. No. 1.7e+05;
1; Mismatches 39
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                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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PN JP 2002
PD 15-JAN-
PF 07-AUG-
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PN JP 20
PD 15-JM.
PF 07-AU
PF 07-AU
PR 05-AU
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GIORDANO
PC C12N1/21,
PC C12N5/00
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C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,
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1 (bases 1 to 171)
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JP 2002010789-A/15409.
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JP 2002010789-A/15409
15-JAN-2002
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05-AUG-1999 US 60/147499
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JP 2002010789-A/15409
15-JAN-2002
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05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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                                                       /organism='Homo sapiens (human)'.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
              organism="Homo sapiens"
|mol_type="genomic DNA"
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Pred. No. 1.7e+05;
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Novel genes, compositions, kits, and methods for identification,
Novel genes, compositions, literapy of breast cancer
Patent: WO 0151628-A 9853 19-JUL-2001,
Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers
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                                                                                        assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 9853 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                       Novel genes, compositions, kits, and methods for identification,
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                       Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                            ocation/Qualifiers
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Pred. No. 1.9e+05;
0; Mismatches 40
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Pred. No. 1.7e+05;
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50; Conserv
                                                                                 Lillie, J., Xu, Y., Wang, Y. and Steinmann, K. Novel genes, compositions, kits, and methods f assessment, prevention, and therapy of breast Patent: WO 0151628-A 1955 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)
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Sequence 1955 from Pater
CQ416921
CQ416921.1 GI:41369150
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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/mol_type="unassigned DNA"
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Pred. No. 1.8e+05;
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Pred. No. 1.9e+05;
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RESULT 38
A58814/c
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Best Local Similarity
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                                             Chrzavzez,E.E. and Aufrere,R.
METHOD FOR DETECTING HEAT-RESISTANT MICRO-ORGANISMS
CONTAMINATING CERTAIN FOOD PRODUCTS
PATENT: WO 9638587-A 3 05-DEC-1996;
ULTRA PROPRE NUTRITION IND REC (FR)
Other publication FR 2734844 961206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chrzavzez, E.E. and Aufrere, R. METHOD FOR DETECTING HEAT-RESISTANT MICRO-ORGANISMS CONTAMINATING CERTAIN FOOD PRODUCTS PATENT: WO 9638587-A 3 05-DEC-1996; ULTRA PROPRE NUTRITION IND REC (FR) Other publication FR 2734844 961206.
                                                                                                                                unidentified unclassified.
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ilarity 59.7%;
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                                 Location/Qualifiers
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/mol_type="unassigned DNA"
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Pred. No. 2.2e+05;
0; Mismatches 29;
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Pred. No. 1.8e+05;
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nes 43; Conserv
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Sequence
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1 (bases 1 to 183)
Chrzarvez nee Taddei, E. and Aufrere,
Method for detecting heat-resistant
contaminating certain food products
Patent: US 6117636-A 3 12-SEP-2000;
Location/Qualifiers
                                                                                              Chrzavzez nee Taddei,E. and Aufrere,R. Method for detecting heat-resistant micontaminating certain food products Patent: US 6117636-A 3 12-SEP-2000;
                                                                                                                                                                                                                                                        Sequence 3 from patent US
AR110714
                                                                                                                                                                                    Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
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                                                     /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="unknown"
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59.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.6; DB 6;
Pred. No. 2.2e+05;
0; Mismatches 29;
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Pred. No. 2.2e+05;
0; Mismatches 29;
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s 6117636.
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No. 2.2e+05;
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micro-organisms capable
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ALU33657/c
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Apteronotus leptorhynchus
Apteronotus leptorhynchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Et
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Gymnotiformes; Apteronotidae; Apteronotus.

1 (bases 1 to 105)
Dimmick, W.W. and Larson, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dimmick, W.W. and Larson, A.

Dimmick, W.W. and Larson, A.

A molecular and morphological perspective on relationships of the otophysan fishes

Mol. Phylogenet. Evol. 6 (1), 120-133 (1996)
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                                                                                                                                      Apteronotus leptorhynchus
U33657
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Apteronotus leptorhynchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Gymnotiformes; Apteronotidae; Apteronotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-AUG-1995) University Boulevard, Lawrence, KS 66045, USA
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U33657
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                                                                                                                                                                                                                                        GGCTACCC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="genomic DNA"
/db xref="taxon:36674"
/tissue_type="muscle"
/note="AC28S4"
                                                                                                                        GI:2443919
                                                                                                                                                                                                                                                                                                                                                                                                                             product="28S ribosomal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Apteronotus
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Pred. No. 2.7e+05;
0; Mismatches 27;
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                                                             Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                            Submitted (26-FEB-2004) Tadashi Shoji, The University of Tokyo, Department of Urban Engineering; 7-3-1, Hongo, Bunkyo, Tokyo 113-8556, Japan (E-mail:shoji@envt.u-tokyo.ac.jp, Tel:81-3-5841-7784, Fax:81-3-5841-8538)
                                                                                                                                                                                                                                                                                                                                                                                                uncultured bacterium uncultured bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uncultured bacterium nirS isolate:DGGE band f2r5-sa.
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Submitted (10-AUG-1995) University
Boulevard, Lawrence, KS 66045, USA
Location/Qualifiers
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Dimmick, W.W. and La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A molecular and morphological perspective on relationships of the otophysan fishes Mol. Phylogenet. Evol. 6 (1), 120-133 (1996) 96426866
                                                                                                                                                                                                                                                                                  Shoji, T
                                                                                                                                                                                                                                                                                                             process using 
Unpublished
                                                                                                                                                                                                                                                                                                                                           Microbial communities
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/gene="nirS"
<1. .>165
                                      /note="PCR products amplified
nirS3R were analyzed by DGGE"
                            1. .165
                                                                                                                        /organism="uncultured bacterium"
/mal_type="genomic DNA"
/isolate="DGGE band f2r5-sa"
/isolation_source="activated slu
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/db_xref="taxon:36674"
/tissue_type="muscle"
/note="AC28S4"
                                                                  country="Japan:Tokyo"
                                                                              environmental
                                                                                               db_xref="taxon:77133"
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                                                                                                                                                                                                                                                                                                                            of an enhanced biological phosphorus removal nitrate and nitrite as electron acceptors
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Pred. No. 2.7e+05;
0; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-FEB-2004) Tadashi Shoji, The University of Tokyo, Department of Urban Engineering; 7-3-1, Hongo, Bunkyo, Tokyo 113-8565, Japan (B-mail:shoji@env.t.u-tokyo.ac.jp, Tel:81-3-5841-7784, Fax:81-3-5841-8538)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 bp Uncultured bacterium nirS gene i isolate: DGGE band f2r5-sa.
AB164173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                process using oxygen, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbial communities of an enhanced biological phosphorus removal process using oxygen, nitrate and nitrite as electron acceptors
 44;
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/transI_table=11
/product="nitrite reductase"
/protein_id="BAD12411.1"
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/tb-xref="GI:45330787"
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                                                                 /protein_id="BAD12411.1"
/db_xreft="G1:4530787"
/translation="YHPEPRVASIVASHYKPEFVVNVKETGQTLLVDYSNVDALKVTTIGTARFLHDGG"
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/mol_type="genomic DNA"
/isolate="DGGE band f2r5-sa"
                                                                                                                        /codon_start=1
/transl_table=11
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                                                                                                                                                                gene="nirs"
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rith wastewater"
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NAL Patent: JP 2002536025-A 29 29-OCT-2002;
THE GENERAL HOSPITAL CORP
OS HOMO SEPIENS (human)
PN JP 2002536025-A/29
PD 29-OCT-2002
PP 01-PEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/24/190
PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU
PC C12N15/09, C07K7/00, C07K14/00, C12Q1/68, C12N15/00 (
T, OT C. S = C OT 9.
FH Key feature (72)
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1 (bases 1 to 123)
Szostak, J.W., Roberts, R.W.
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09-FEB-1999 US 09/247190
JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00
                                                                                                                                                                    Conservative
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/db_xref="taxon:9606"
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 bp DNA linear GSS 17-DEC-20 pacs2-164_6657.x1 pacs2-164_Pseudomonas aeruginosa genomic clone pacs2-164_6657, genomic survey sequence.
Spencer, D.H.,
                                                           Pseudomonas aeruginosa
Pseudomonas aeruginosa
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                            Bacteria; Proteobacteria; Gamm
Pseudomonadaceae; Pseudomonas.
                                                                                                       BZ566906.1
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Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonadaceae; Pseudomonas.
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole
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/mol_type="genomic DNA"
/strain="2-164"
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                                                                                                                                                                    Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

This sequence has been generated in the framework of the french
                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                 plant genomics programme 'Genoplante' (ht
and http://genoplante-info.infobiogen.fr)
    Location/Qualifiers
                                                                                                                                                                                                                                                                                    Genoplante, a major
Unpublished (2003)
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Triticum aestivum (bread wheat)
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CD931316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 2062216954
Fax: 2066857244
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Whole-Genome-Sequence variation among multiple isolates
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                      Contact: Genoplante
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Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris K. Raymond
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                            /tissue_type="grain
pollination) "
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/note="clinical isolate 2-164
                                                           /db_xref="taxon:4565"
/clone="GR45114C04"
                                                                                         /mol_type="mRNA"
/cultivar="recital"
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Location/Qualifiers
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/cultivar="recital"
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'clone="GR45114C04"
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Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1878)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., W
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the
its comparison to Arabidopsis
                                                                                                                                                                                                                                                                                           Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
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OBIFCC045611 Oryza sativa Express Library Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzaa.
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Chinese Academy of Sciences, E
Tel: 86-10-80481559
Fax: 86-10-80488676
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Unpublished (2004)
Contact: Chen Chen
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Jiao,Y., Sun,N., Zhang,X., Bao,J.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regu
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Rice genomic sequence.
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/db_xref="taxon:39946"
/clone_lib="Oryza sativa
/note="Oryza sativa exon
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_mol_type="genomic DNA"
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, Sun,D., Zhao,H., Yuan,
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Zhao,H., Yuan
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-NN1155-
2711000-628-a09&t3=2000-10-27&t4=1)
Seq_primer: puc 18 forward
                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF945949
CM0-NN1155-271000-628-a09
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
Tel: 86-10-80481559
                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chenchen@genomics.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/mol_type="genomic DNA"

/db_xref="taxon:39946"
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Pred. No. 23;
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                                                                                                                                  This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-NN1155-271000-628-a09&t3=2000-10-27&t4=1)
                                                                                                                                                                                                 Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                   Seq primer: puc 18 forward
                                                                                                                                                                                                                                      Tel: +55-11-2704922
                                                                                                                                                                                                                                                                     Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                       Rua Prof. Antonio
                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
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Location/Qualifiers
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quality sequence stop: 175
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
               /organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
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Unpublished (2003)
Contact: Genoplante
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                                                                                                                                                                                                                  /tissue_type="grain (174 degrees per day after
pollination)"
/clone_lib="G174"
                                                                                                                                                                                                                                                                                           /cultivar="recital"
/db_xref="taxon:4565"
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Genoplante, a major partnership french
Unpublished (2003)
Contact: Genoplante
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genomic survey sequence.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fra Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other GSSs: BOMQF14TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
                                                                             Email: cdtown@tigr.org
DNA is from a doubled haploid provided
Seq primer: TF
                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                         BOMQF14TF BO_2_3_KB Brassica oleracea genomic clone BOMQF14
                                                                                                                                                                                                                                                                                                                                    Brassica oleracea
                                                              Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
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Class: sheared ends.
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Fax: 301-838-0208
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                                                                                                                                           Medical Center Drive, 301-838-3523
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/organism="Brassica oleracea"
/mol_type="genomic DNA"
                                            Location/Qualifiers
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/clone_lib="BO_2_3 KB"
/clone="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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Genome Sequencing Center
Washington University School of Medi
Email: submissions@watson.wustl.edu
plare: odq84 row: c column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole genome shotgun reads from Brassica oleracea 
Unpublished (2002)
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                   /note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica Oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                      /organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
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/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                           clone_lib="B.oleracea002"
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/db_xref="taxon:3712"
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   Score 36.4; DI
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg84 row: c column: 07
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Richard K. Wilson
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odg84c07.gl B.oleracea002 Brassica
 BZ427562
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                                                                                 GCCGAG 405
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                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:3712"
/db="B.oleracea002"
/clone lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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           1 (bases 1 to 818)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BONJT45TF
                                                                                               Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                      BONJT45TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONJT45, genomic survey sequence.
Contact:
                                                                                                                                                                                 Brassica oleracea
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                                                                                                                                                                                                                     BZ427562.1 GI:26669268
                                                                                                                                                                                                                                      BZ427562
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DNA is from a doubled |
Seq primer: TR
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Unpublished (2001)
Other GSSs: BONUT45TF
Contact: Chris Town
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Fax: 301-838-0208
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/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"
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/mol_type="genomic DNA"
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/clone="BONJT45"
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Be
Tel: 86-10-80481559
Fax: 86-10-80488676
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DNA is from a doubled
Seq primer: TR
Class: sheared ends.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Foales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                          Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CL980758 834 bp DNA linear GSS OSIFCC045376 Oryza sativa Express Library Oryza sativa
                                                                                                                                                                                        Email: chenchen@genomics.org
                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CL980758.1 GI:52416004
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Fax: 301-838-0208
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          /clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
                                                                                                                                 Location/Qualifiers
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/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb shea:
total DNA inserted into pHOS1 using BstXI linkers"
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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349 GCGCCG
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 834)
Ma_L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
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                                                                                                                                                                                                                                                                                                                                                                                                            Email: chenchen@genomics.org.cn
                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 86-10-80488676
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CL980758
CL980758.1 GI:52416004
GSS.
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Location/Qualifiers
                                                                                                                                                                                                                                                                 oxganism="Oryza sativa (i
/mol type="genomic DNA"
/db xref="taxon:3946"
/clome lib="Oryza sativa E
/note="Oryza sativa exon t
344
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Pred. No. 34;
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041B18 of
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                               627 bp DNA linear GSS 01-SEP-; nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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                                        AZ933792.1 GI:13775852
GSS.
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria, Proteobacteria, Alphaproteobacteria;
Bacteria, Proteobacteria;
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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50; Conserv
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Tomkins, J.P.,
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/db_xref="taxon:99883"
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BJ_Ba0001E22f B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence.
AZ933792
AZ933792.1 GI:13775852
GSS.
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Clemson University
100 Jordan Hall, Clemson, SC
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A marker-dense,
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Fax: 864 656 4293
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Bradyrhizobium japonicum
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                                                                                                  Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                               genome
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Class: BAC ends
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100 Jordan Hall, Clemson,
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/lab_host="B. coll"
/clome_lib="B. japonicum_BAC_library"
/note="Yector: pIndigo536; Site_1: Hi
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/mol_type="genomic DNA"
/strain="USDA110"
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organism="Bradyrhizobium"/
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                          ocation/Qualifiers
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Tetraodon nigroviridis genome survey sequence T7 end of clone
063118 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                         - Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as scale clone-end sequencing project of the Terraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                Location/Qualifiers
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/db_xref="taxon:99883"
note="Genoscope sequence ID : COBG063BE09LP1~end
                                                          'clone="063I18"
                                                                                                                    organism="Tetraodon nigroviridis"
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                        28
                                                                                                                                                                                                                                                                                        This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) Genoscope - Centre National de Sequencaç BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.
                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope.
Direct Submission
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                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:99883"
/clone="063I18"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 862)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anam-Dong, Seongbuk-Gu,
Tel: +82 2 3290 3005
Fax: +82 2 3290 3501
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                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="5MT resistant rice mutant cDNA library" /note="Vector: pBluescripts SK(+/-) phagemid; The rice mutant resistant to growth inhibition by 5MT were selected from the callus irradiated with gamma ray of 50 gy through rice cv. Donganbyeo embryo culture.For construction of the cDNA library, 5MT resistant homologous rice mutants were treated by 5MT for 3 weeks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultiva /mol type="mrNa" /mol type="mrNa" /cultiva="Douganbyeo" /db_xref="taxon:39947" /tlssue_type="5MT treated leaves, stems, /dev_stage="seedling grown for 3 weeks" /lab_host="XL1-Blue_MRF'"
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a; Poales; Poaceae;
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LOCUS DEFINITION

CO435934 862 bp
OBMR568 SMT resistant rice mutant

mRNA linear F

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RESULT 27
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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CO435934.1 GI:53552954
Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                AL306353.1 GI:8204690
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                            Tetraodon nigroviridis genome survey sequence T3 end 013I12 of library A from Tetraodon nigroviridis, geno
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| 72; | Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance in mutant rice Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anam-Dong, Seongbuk-Gu,
Tel: +82 2 3290 3005
Fax: +82 2 3290 3501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="5MT resistant rice mutant cDNA library" /note="Vector: pBluescripts SK(+/-) phagemid; The rice mutant resistant to growth inhibition by 5MT were selected from the callus irradiated with gamma ray of 50 Gy·through rice cv. Donganbyeo embryo culture.For construction of the cDNA library, 5MT resistant homologous rice mutants were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treated by SMT for 3 weeks."
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/tissue_type="SMT treated leaves,
/dev_stage="seedling grown for 3 w
/lab_host="XL1-Blue_MRF/"
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/mol_type="mRNA"
/cultivar="Donganbyeo"
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RESULT 28
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Bernot, A., Fizames, ...

Saurin, W. and Weissenbach, J.

Saurin, W. and Weissenbach, J.

Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence war Genet. 25 (2), 235-238 (2000)
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a larg
scale clone-end sequencing project of the Tetracdon migroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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/mol type="genomic DNA"
/db xref="teaxon:99883"
/clone="013112"
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                                                                                                             Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
                                                                                                                                                                                   1 (bases 1 to 367)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources
Unpublished (2001)
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                        Invergowrie, Dundee, DE
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGAGACGTCCTCCGCCGACGAGACCATGAGCGAG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGAGTCGGCGGCCGACTCGACGATGAGCGAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCTCCTNGGGTCGGACGATGTCCGGGAGCCGGCCGCCTNTGCTGTTCTNGCGCCTGT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
_SQ010_K07_R root, 3 week,
m vulgare subsp. vulgare c
                                                        est@scri.sari.ac.uk.
organism="Hordeum vulgare subsp. vulgare"
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                               Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="013I12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Genoscope sequence ID : C1AA003ZE01A1~end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone lib="A"
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60.0%;
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Pred. No.
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u,L., Billault,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    stressed, cv Optic,
EBro08_SQ010_K07 5
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nigroviridis
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RESULT 30
BQ767987/c
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                             TOURNAL
                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 GTCCGTGGGCCGCCGGCCGACACGCCGACGTCGCACCCGGTCTGCCTCTGCCGCCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
                                                                                                                                                                                                                                                                                                                                           Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudi
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,
Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                             Genome Dynamics/Computational Biology Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotlan Tel: 00 44 1382 562731

Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EBro08_SQ010_K07_R root, Hordeum vulgare subsp. v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ767987.1
                                                                                                                                                                                                                                                                                                                            Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                            est@scri.sari.ac.uk.
/db_xref="taxon:112509"
/clone="EBroO8 SQ010 K07"
/tissue_type="Toot"
/dev_stage="3 week"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
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                                                                                                                 /mol_type="mRNA"
/cultivar="Optic"
                                                                                                  /sub_species="vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="BBro08_SQ010_K07"
/tissue_type="root"
/dev_stage="3_week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sub_species="vulgare"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Optic"
                                                                                                                                                       organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                          ocation/Qualifiers
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Pred. No. 4
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3 week,
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                                                                                                                                                                                                                                                                     Scotland,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA linear drought-stressed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stressed, cv Optic, EBro08
EBro08_SQ010_K07 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 367;
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augh,R.
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EV Optic, EBro08
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3 week,

drought-stressed,

cv Optic,

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RESULT 31
CE011375
LOCUS
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AUTHORS
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                                                                                                                            ORIGIN
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                                                            Query Match
Best Local S
Matches 68
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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tigr-gss-dog-17000321027441 Dog
genomic survey sequence.
CE011375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS
                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 397)
Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CE011375.1 GI:35014076
                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kirkness EF
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                      14512627
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                                                                             Similarity
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                          GTCGGCGGCCGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGA
 GTCGGCGGGTGGGGGGCGTCAGAGGCGGTGTCGGGGGAGGCGGCTCCAGAGATGGCAG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                              23.1%;
.larity 55.7%;
Conservative
                                                                                                                                                                                                                                                                                         shotgun.
                                                                                                                                                                                                                                                                                                        ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: psport; Site 1: Sal 1; Site 2: Not 1; Non-normalised library, directionally cloned into psport. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Function) project.
                                                                                                                                           /db xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_l: BstXI; Libraries were prepared
peripheral blood"
                                                                                                                                                                                                                       organism="Canis familiaris"
/mol_type="genomic_DNA"
                                                                                                                                                                                                        strain="Standard Poodle"
                                                                                                                                                                                                                                                                          ocation/Qualifiers,
                                                                                                                                                                                                                                                            .397
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Pred. No. 49;
0; Mismatches
                                                            Score 35.6; D. Pred. No. 55; 0; Mismatches
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                                                                                              ВB
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                                                                                              9;
                                                                54;
                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive
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                                                                                                Length 397;
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                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                 Gaps
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VERSION KEYWORDS

CB682412 CB682412.1 EST.

ACCESSION

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REFERENCE
AUTHORS
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VERSION
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                                           RESULT 33
CB682412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
Tel: 301-838-0200
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tigr-gss-dog-17000321027441 |
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Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Frase
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 397)
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CE011375.1 GI:35014076
CB682412 624 bp mRNA linear EST 09-JOSJNEF09L11.f OSJNEF Oryza sativa (japonica cultivar-group) clone OSJNEF09L11 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 301-838-0208
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/note="Site 1: BstXI; Libraries were prepared
peripheral blood"
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/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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55.7%;
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Fraser,C.M. and
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                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                            OSJNEf09L11.f OSJNEf Oryza sativa (japonica cultivar-group) clone OSJNEf09L11 5', mRNA sequence.
CB682412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
     Unpublished (2003)
Contact: Rod Wing
Arizona Genomics I
                                                       Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
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BACKWARD: gga aac agc tat gac cat g
Plate: 09 row: L column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between rice and Magnaporthe grisea Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85721-0088, USA
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                                                                                                                               (bases 1 to 624)
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/mol_type="mRNA"
/cultivar="Nipponbare"
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/dev_stage="3 week"
/lab_host="DH10B"
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/note="Vector: pBluescript
/hoI; Uninfected Control"
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/clone="OSJNEf09L11"
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                                                                                                        Bmail: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
                                                                                                                                                                                    Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Camp
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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5', mRNA sequence.
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Location/Qualifiers
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Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
                                                                        Plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/note="Vector: pBluescript
XhoI; Uninfected Control"
                                                       Location/Qualifiers
/organism="Saccharum
/mol_type="mRNA"
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Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Saccharum; Saccharum officinarum
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Biological Sciences West, 448A, P.O.
85721-0088, USA
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Boacharum officinarum
                                                                                                                                                                              Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
                                                                                                                                                                                                                                                    Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                     Vettore,A.L., da Silva,F.R., Kemper,E. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5', mRNA sequence.
CA198784
CA198784.1 GI:35230393
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SCCCST3C12B03.g ST3 Saccharum
                                                                                                                                                                                                                                    Email: parruda@unicamp.br
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/db_xref="taxon:4547"
/clone="SCCCST3C12B03"
'note="Organ:
                   'lab_host="DH10B"
'clone_lib="ST3"
                                                                                                organism="Saccharum officinarum"
                                                                                                                                  location/Qualifiers
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/clone="SCCCST3C12B03"
/lab_host="DH10B"
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Pred. No. 54;
 Fourth apical stalk internodes
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eukariomycetidae; Sordariales; Sordariaceae;
Sordariomycetidae; Sordariales; Crawford M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L., Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E., Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S.
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NCW01B11T3 Westergaards
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                             Department of Biology
University of New Mexico
Castetter Hall, Albuquero
                                                                                                                                                                                                                                                                                                                                                                                                        9290248 Contact: Natvig, D.O./Nelson, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequences from conidial, mycelial, Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)
                                                                                                                                                                                                                                                                                                                              Tel: 505 277 3411
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Location/Qualifiers
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/tissue_type="Unfertilized sexual tissue"
/dev_stage="Unfertilized sexual stage"
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                                                                                                                                         /db_xref="taxon:5141"
/clone="worner:"
                                                                                                                                                                          /organism="Neurospora crassa"
/mol_type="mRNA"
/strain="74-OR23-IV A (FGSC 2
                                                                                                                                       clone="W01B11"
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Pred. No. 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Natvig, D.O./Nelson, M. Department of Biology University of New Mexico Castetter Hall, Albuquerque, N Tel: 505 277 3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson, M.A., Kang, S., Braun, B.L., Crawford, M.B., Dolan, P.J.
Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S., Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      ngp@biology.unm.edu.
                                                                                        /clone lib="Westergaards" /clone lib="Westergaards" /clone="Vector: pBlueScript SK (-); Site 1: EcoR1; Site 2 XhoI; Westergaard's medium (Nitrogen limiting). Floating mycelial mats grown at 25C for 36 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
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                                                                                                                                                                                                         /sex="Mating type A"
/tissue type="Unfertilized sexual tissue"
/dev stage="Unfertilized sexual stage"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                  /strain="74-OR23-IV A
/db xref="taxon:5141"
/clone="W01B11"
                                                                                                                                                                                                                                                                                                                                           organism="Neurospora crassa"
|mol_type="mRNA"
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                   23.0%;
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0; Mismatches
                   Score 35.4;
Pred. No. 61;
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   Mismatches
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Blueyes, E.,
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W01B11 5',
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CA227997
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Matches
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                                           324 GCCGACCAGCCAGGGCCTCCTTCACAACGTCGAGCGAGATGTCCATCTCGGCGACCCTC 383
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                                                                                                                                                                                                           78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centro de Biologia Molecular e Engenharia
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
Tel: 55 19 3788 1137
Pax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Saccharum; Sacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: parruda@unicamp.br
Clone distribution: clone Collection
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
Plate: 015 row: B column: 05
Seq primer: SP6 Promoter primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vettore, A.L.,
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                                                                         ATCGTCGAGTCGGCGGCGGCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGA 121
  CTCGACGATGAGCGAGATGACCAGCTCCG 150
                                                                                                                                                   GGCCGGAGCTGGTCATCTCGCTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTC
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                                                                                                                             GGCCTCTCCTGAGGCTGAGGCCCGGCGACGGGCGGGGCTGGCACGCTGGTCTTCCTCACC 323
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                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Saccharum officinarum FL3"
/noce="Organ: Base of developing inflorescence (5cm-long);
/vector: pSportl; Site 1: Sall; Site 2: Notl; An
unidirectional cDNA library generated from [Base of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharum officinarum"
/ml_type="mRNA"
/db xref="taxon:4547"
/clone="SCJLFL3015B05"
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Pred. No. 6:
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la: Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                  Length 704;
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AUTHORS
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Plate: 015 row: B column: 05
Seq primer: SP6 Promoter primer.
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Clone distribution: clone distribution
through the Brazilian Clone Collection
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vettore, A.L., da Silva, F.R., Kemper, E.L. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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                                                                                                                                                                   GECGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGA 132
                                                                                                                                                                                                           Saccharum officinarum
                                                       GCCTCAGCCTCAGGAGAGGCC 264
                                                                                             GCGAGATGACCAGCTCCGGCC 153
                                                                                                                                 GTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTC 72
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                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long);
/note="Organ: Base of developing inflorescence (5cm-long);
/vector: pSportl; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [Base of
developing inflorescence (5cm-long)]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 KD were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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/db_xref="taxon:4547"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                 23.0%;
                                                                                                                                                                                                                                                                                                                 Score 35.4;
Pred. No. 61;
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RESULT 42
BF483067/c
                                                                                                    DEFINITION
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                           BF483067 441 bp mRNA linear EST 06-DEC-20 MHE2314_D05_G10ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2314_D05_G10, mRNA sequence.

BF483067 BF483067.1 GI:11566368
EST.
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1 (bases 1 to 441)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence with phred score
Seq primer: Stratagene SK primer.
Location/Qualifiers
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Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
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441 bp mRNA linear EST 06-DEC-2000 WHE2314 D05 G10ZS Wheat pre-anthesis spike cDNA library Triticum cDNA clone WHE2314 D05 G10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                 CGACGATGAGCGAGATGACCAGC 109
                                                                                                                                                                                                                                                    CGGCCÁGGGGCGACGGCAACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli SOLR"
/clone lib="Wheat pre-anthesis spike cDNA library"
/clone lib="Wheat pre-anthesis spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site I: BcoRI; Site 2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, gr
and yellow anther were collected and total RNA, and
are spike with awns total RNA, and are spike with awns the spike with awns total RNA, and are spike with awns the spike with awns total RNA, and are spike with awns total RNA, and are spike with awns to the spike with awns trimmed, white, gr
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/rissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E__coli_SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Chinese Spring"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ions and DNA sequencing were performed
lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>0</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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78;
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20
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KEYWORDS

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REFERENCE
AUTHORS
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BQ805125
                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                                                            571 bp mRNA linear EST 31-JUL-: WHE3563_B09_C17ZS Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3563_B09_C17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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1 (bases 1 to 441)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Anderson,O.B., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
Seaton,C.L. and Tong,J.C.
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Triticum aestivum
  1 (bases 1 to 571)
Altenbach, S., Ander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Strategene SK primer.

Location/Qualifiers
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                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                    Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000
                                                Pooideae; Triticeae; Triticum.
                                                                                                                                          Triticum aestivum (bread wheat)
                                                                                                                                                                                           BQ805125.1 GI:22029334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                          GACGGCCGCCCCCCCCCACG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCTCCGGCCGCCGACTCGACG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGGTCATCTCGCTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGAC 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Wheat pre-anthesis spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="WHE2314_D05_G10"
/clssue_type="Spike_before anthesis"
/dev_stage="Adult plant"
/lab_host="E_coli_SOLR"
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/cultivar="Chinese_Spring"
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63.9%;
    Anderson, O.D., Chao, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 441; Pred. No. 78;
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    Chin, A., Close, T.J.,
                                                                                                                                                                                                                                                                                     EST 31-JUL-2002
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  LOCUS
DEFINITION
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                                              BQ805125/c
                                                                        RESULT 44
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                                                                                                                                                                                                                                         116
BQ805125 571 bp mRNA linear EST 31-JUL-WHE3563_B09_C17ZS Wheat developing grains cDNA library Triticum
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Local Similarity
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West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomes - Developing grains cDNA library
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The structure and function of the expressed portion of the wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 5105595818
                                                        CGACGATGAGCGAGATGACCAGC 109
                                                                                                                          CGGCCAGGGGCGACGGCAACGGC 198
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 well-watered, without post-anthesis fertilizer, Environment 3) 370C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, with post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the CDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda ZAP II, excised phagemid; Site_1
coRI; Plants were grown under six following different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fertilizer, Environment 2) 24oC/17oC day/night,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Wheat developing grains cDNA library"
/note="Vector: Lambda ZAP II, excised phagemid; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dev_stage="3-44 days post anthesis seed"
lab_host="E. coli SOLR"
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/tissue_type="whole grains"
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/cultivar="Butte 86"
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                                                                                                                                                                                                                                                                                                              Length 571;
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Matches Query Match

Local

Similarity

22.7%;

DB 5;

Length 571

Conservative

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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 571)
Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J.,
Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J.,
Rausch, C.J., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aestivum cDNA clone WHE3563_B09_C17, mRNA sequence.
BQ805125
BQ805125.1 GI:22029334
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences have been trimmed quality sequence with phred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800 Buchanan Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
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                                                                                                                                                                                                                                                                                    well-watered, without post-anthesis fertilizer, Environment 3) 370c/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370c/170c day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370c/170c day/night plus drought, with post-anthesis fertilizer, Environment 6) 370c/170c day/night plus drought, without post-anthesis fertilizer, Environment 6) 370c/170c day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment dat 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 
                                                                                                                 CDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescribt SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside, Plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clome lib="Wheat developing grains cDNA library" /note="Vector: Lambda ZAP II, excised phagemid; Site_1 EcoRI; Plants were grown under six following different environmental regimes in greenhouse, Environment 1 240C/17oC day/night, well-watered, with post-anthesis fertilizer, Environment 2) 24oC/17oC day/night,
                                    preparations and DNA Anderson lab (others)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4565"
/clone="WHE3563_B09_C17"
/tissue_type="whole_grains"
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/lab_host="E. coli SOLR"
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                      University of California, Riverside. Plass
parations and DNA sequencing were performed
erson lab (others)."
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REFERENCE
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KEYWORDS
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BG279219
Search completed: April
Job time : 3133 secs
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Kupfer,D., Lai,H., Nelson,M. and Roe,B.
ESTS from a Neurospora crassa Sexual cDNA Library
Unpublished (2001)
Other ESTs: blf04np.fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG279219
430 bp mRNA linear EST 21-FEB-2: blf04np.rl Neurospora crassa sexual cDNA library, Uni-zap vector system Neurospora crassa cDNA clone blf04np 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact Dr. Mary Anne Nelson, Department of Biology, University of New Mexico, Albuquerque, NM 87131 (e-mail address manelson@unm.edu) regarding clone availability seq primer: Mi3 Universal Reverse Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, Uni
620 Parrington Oval, Norman, OK 73019, USA
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                                                                                                                CCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGACTCGAC 127
                                                                                                                                                        CCGCGGGTACCAGTACCAGTCTCATACTCAGCCCCAGCCGGACAGTGGCC
                                                                                                                                                                                            CTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                            /note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                          vector system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Neurospora/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="Neurospora"
                                                                                                                                                                                                                                                                                                                                                                                                                                              dev stage="sexual"
/lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="blf04np"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="wild type"
db_xref="taxon:5141"
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                    2005,
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Pred. No. 87;
0; Mismatches
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Result
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Maximum DB
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Perfect score:
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US-10-37-963-5171

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RESULT 2
US-09-887-194A-13/c
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09887194A
Publication No. US20030036197A1
GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THE
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SEQ ID NO 13
LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION:
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CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
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illarity 100.0%;
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Pred. No. 2.2e-37;
); Mismatches 0;
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Sequence 11328, A
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Sequence 5073, App
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APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hitz, William D
APPLICANT: Hitz, William D
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 154
TYDEP: DNA
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                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: region of pKS133 US-09-934-900-25
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US-09-934-900-25
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                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
                                                                                                                                                                       Matches
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Best Local Similarity
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APPLICANT: Stecca, Kevin L.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: BECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION FILE REFERENCE: BB1449 US NA
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                   100.0%; Score 154; DB 10; 100.0%; Pred. No. 2.2e-37; tive 0; Mismatches 0;
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RESULT 5
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US-09-934-900-25/c
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                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MCGONIGIE, Brian
APPLICANT: MCGONIGIE, BRIAN
TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US // 10/734,947
CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
                                                                                   SEQ ID NO 7
LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10734947
Publication No. US20040128714A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/22696
PRIOR APPLICATION NUMBER: 60/22696
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
                                                                                                                        CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary OTHER INFORMATION: region of pKS133
-09-934-900-25
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                                       ORGANISM: Artificial Sequence
                                                                 TYPE: DNA
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OTHER INFORMATION: Artificial sequence containing a NotI site flanked by two
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Yadav, Naren
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Hitz, William D
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US-10-981-293-25
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                                                                                                                                                                                                                                                 RESULT 7
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Best Local S
Matches 154
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                                                                                                                                                 Sequence 25, Application US/10981293 Publication No. US20050066390A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 154; Conserv
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SEQ ID NO 7
            APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McGonigle, Brian

TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO O
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
CURRENT APPLICATION NUMBER: US/10/734,947

CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
PRIOR FILING DATE: 2002-12-13
PRIOR FILING DATE: 2002-12-13
PRIOR FILING DATE: 2002-12-13
                                                                         APPLICANT: Booth, Russ
APPLICANT: Cahoon, Re
APPLICANT: Hitz, Will
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hes 154;
CANT: Kinney, Anthony
CANT: Yadav, Naren
OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
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Hitz, William D
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100.0%; Pred. No. 2.2e-37;
tive 0; Mismatches 0;
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Pred. No. 2.2e-37;
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CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
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                                                                                                                                         ; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-981-293-25
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                                                                       Matches
                                                                                        Query Match
Best Local :
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/9/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER CECTATOR
                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Office 97
EQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: BB1476 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleotide Sequences of a New TITLE OF INVENTION: ACP Desaturase
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                                                                                                                                                                                              LENGTH: 154.
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: DNA
ORGANISM: Artificial Sequence
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     154
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Hitz, William D
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Yadav, Naren
                                                                       Conservative
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                                                                   Score 154; DB 19;
Pred. No. 2.2e-37;
; Mismatches 0;
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Pred. No. 2.2e-37;
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TITLE OF INVENTION METHOD TO INCREASE THE I TITLE OF INVENTION: PRODUCING INCREASED LEV FILE REFERENCE: BB1526 US NA CURRENT APPLICATION NUMBER: US/10/459,159 CURRENT FILING DATE: 2003-06-11 PRIOR APPLICATION NUMBER: 60/388,280 PRIOR APPLICATION NUMBER: 60/388,280 PRIOR FILING DATE: 2002-06-13 UNDBER OF SEQ ID NOS: 10 SOFTWARE: Microsoft Office 97 SEQ ID NO 1
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                        APPLICANT: MCGORIGIE, Brian
APPLICANT: MCGORIGIE, Brian
APPLICANT: MCGORIGIE, JOAN T.
TITLE OF INVENTION: METHOD TO INCREASE THE ISOFLAVONOID LEVELS IN PLANTS;
TITLE OF INVENTION: PRODUCING INCREASED LEVELS OF ISOFLAVONOIDS
FILE REFERENCE: BB1526 US NA
CURRENT PLILICATION NUMBER: US/10/459,159
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 60/388,280
PRIOR APPLICATION NUMBER: 60/388,280
PRIOR APPLICATION NUMBER: 60/388,280
PRIOR TILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
LENGTH: 7701
TENGTH: 7701
                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10459159
Publication No. US20040006795A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: McGonigle, Brian
APPLICANT: Odell, Joan T.
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ORGANISM: expression vector pKS151
                      TYPE: DNA
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LOCATION: (6516)..(6516)
OTHER INFORMATION: n = A,
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ORGANISM: expression vector
FEATURE:
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RESULT 12
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; LOCATION: (6516).. (6516)
; OTHER INFORMATION: n = A,
US-10-459-159-1
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APPLICANT: Hession, Aideen O.

TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL PILE REFERENCE: B81523 US NA
CURRENT APPLICATION NUMBER: US/10/427,570A
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: 60/379,361
PRIOR PRILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 7701
Sequence 9, Application US/10427570A Publication No. US20040010818A1 GENERAL INFORMATION:
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Publication No. US20040010818A1
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Best Local :
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APPLICANT: Maxwell, Carl A
APPLICANT: Hession, Aideen
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Unsure LOCATION: (6516) OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Similarity 100.0%;
54; Conservative 0
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Pred. No. 1.8e-37;
); Mismatches 0;
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Pred. No. 1.8e-37;
; Mismatches 0;
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                                                                         ; NAME/KEY: misc feature
; LOCATION: (6516)..(6516)
; OTHER INFORMATION: n = A
US-10-734-947-1
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US-10-734-947-1
                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 7701
TYPE: DNA
ORGANISM: Artificial Sequence
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SEQ ID NO 9
LENGTH: 7701
   Matches 154;
                                      Query Match
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McGonigle, Brian
TITLE OF INVENTION: MCTHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
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CURRENT APPLICATION NUMBER: US/10/427,570A
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: 60/379,361
PRIOR FILING DATE: 2002-05-09
PRIOR FILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 9
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APPLICANT: Hession, Aideen O.
TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL
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APPLICANT: Maxwell, Carl A
APPLICANT: Hession, Aideen
                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Expression
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ORGANISM: Artificial Sequence
FEATURE:
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                   Local Similarity
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 Score 154; DB 18;
Pred. No. 1.8e-37;
; Mismatches 0;
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Pred. No. 1.8e-37;
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CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60

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; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (6516).. (6516)

; OTHER INFORMATION: n = A,

US-10-734-947-1
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US-09-906-209-17
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US-10-734-947-1/c
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Publication No. US20040128714A1

GENERAL INFORMATION:

APPLICANT: McGonigle, Brian

TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE

TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE

TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES

FILE REFERENCE: BB1535 US NA

CURRENT APPLICATION NUMBER: US/10/734,947

CURRENT TILING DATE: 2003-12-11

PRIOR APPLICATION NUMBER: US 60/433,433

PRIOR FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Microsoft Office 97

SEQ ID NO 1
                                                          GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: llag, Lawrence L.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                          Sequence 17, Application US/09906209
Patent No. US20020165385A1
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Best Local :
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PRIOR APPLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                          US-09-934-900-26
                                                                                                                          RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                     US-09-906-209-17
GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rel
APPLICANT: Hitz, Willi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION UNMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09906209
Patent No. US20020165385A1
GENERAL INFORMATION:
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SEQ ID NO 17
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                                                                      Sequence 26, Application US/09934900 Publication No. US20030054521A1
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APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: Ilag, Lawrence L.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB1451 NA
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TYPE: DNA
ORGANISM: synthetic
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LOCATION: (3951)
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LOCATION: (3951)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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112; Conserv
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                                                                                                                                                                                                                                                                               43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
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Pred. No. 9.8e-25;
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APPLICANT:

Cahoon, Rebecca Hitz, William D Kinney, Anthony

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SEQ ID NO 26
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LENGTH: 6611
TYPE: DNA
ORGANISM: Plasmid pBS68
                                                                                                         Matches
                                                                                                                                         Query Match
                                                                                                                                                                         NAME/KEY: Unsure
LOCATION: (4436)..(4436)
OTHER INFORMATION: n = A
-09-934-900-26
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Best Local Similarity 97.7%;
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TYPE: DNA
ORGANISM: Plasmid F
FEATURE:
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CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Yadav, Naren
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APPLICANT: Cahoon, Re
APPLICANT: Hitz, Will
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TITLE OF INVENTION: ACP Desaturase
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NAME/KEY: Unsure
LOCATION: (4436)..(4436)
OTHER INFORMATION: n = A,
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     ATGAGCGAGATGACCAGCTCCGGCCG 154
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                                        Cahoon, Rebecca
Hitz, William D
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Pred. No. 7e-16;
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                                                                                      APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
TITLE OF INVENTION: ACP Desaturase
TITLE OF INVENTION: ACP Desaturase
TITLE OF INVENTION: 200 Desaturase
TITLE OF INVENTION: 2004-11-04
PRIOR APPLICATION UNMBER: US/09/934,900
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR APPLICATION UNMBER: 00/09/934,900
PRIOR APPLICATION UNMBER: 00/09/934,900
PRIOR APPLICATION UNMBER: 00/09/934,900
PRIOR APPLICATION UNMBER: 00/09/934,900
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOPTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 6611
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SEQ ID NO 26
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Publication No. US20050066390A1
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APPLICANT: Kinney >--'
APPLICANT: Kinney >--'
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APPLICANT: Cahoon, Rebecca
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
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LOCATION: (4436)...(4436)
OTHER INFORMATION: n = A
NAME/KEY: Unsure
                        LENGTH: 6611
TYPE: DNA
ORGANISM: Plasmid pBS68
FEATURE:
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ORGANISM: Plasmid pBS68
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Yadav, Naren
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RESULT 22
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US-09-887-194A-29
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LENGTH: 963
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local S
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Publication No.
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
                                                                                          APPLICANT:
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APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
SOFTWARE: Microsoft Office 97
                           CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
                                                                     APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
                 NUMBER OF
                                                         FILE REFERENCE: BB1449 US NA
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OTHER INFORMATION: n = A
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                                                                                                                   Kinney, Anthony
Lowe, Keith S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description of Artificial Sequence: region of pKS149
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100.0%; Pred. No.
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Pred. No. 7e-16;
0; Mismatches
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2.7e-15;
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SEQ ID NO 12
LENGTH: 80
                                                                                                        GENERAL INFORMATION:
                                                                                                                      Sequence 12, Application US/09887194A Publication No. US20030036197A1
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LENGTH: 963
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APPLICANT:
TITLE OF IN
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                                                                         APPLICANT: Glassman, APPLICANT: Gordon-Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
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                              APPLICANT:
                                                APPLICANT:
                                                              APPLICANT:
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: region of pKS149
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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mes 80; Conserv
 OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
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                                        Gordon-Kamm, Wil
Kinney, Anthony
Lowe, Keith S.
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Lowe, Keith S.
                           Nichols,
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                 Kevin L.
                              Scott E.
                                                                                         Kimberly F
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Pred. No. 6.3e-1:
0; Mismatches
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Pred. No.
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. 2.7e-15;
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CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
RESULT 26
US-09-934-900-24/c
US-09-934-900-24/c
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
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SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 80
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/226996 PRIOR FILING DATE: 2000-08-22
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                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS106 and pKS124
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OTHER INFORMATION:
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80; Conservative
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Yadav, Naren
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Hitz, William D
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100.0%; pr
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6.3e-15;
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GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
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SOPTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 80
TYPE: NO.
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SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 80
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                                                                                                         Query Match
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Best Local Similarity
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CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
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                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS106 and pKS124
                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                    Local Similarity
les 80; Conserv
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Yadav, Naren
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Hitz, William D
                                                                      Conservative
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                                                                                     Score 80;
Pred. No.
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Pred. No. 6.3e-15;
                                                                      Mismatches
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                                                                                     DB 19; 1
. 6.3e-15;
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                                                                                               NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09887194A
Publication No. US20030036197A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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SEQ ID NO 24
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OTHER INFORMATION: Description of Artificial Sequence: 09-887-194A-14
                                                                                                                                                                               APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND
FILE REFERENCE: BB1449 US NA.
                                                                                                                                                                                                                                                       APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
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APPLICANT:
APPLICANT:
                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/887,194A CURRENT FILING DATE: 2002-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl TITLE OF INVENTION: ACP Desaturase FILE REFERENCE: BB1476 US NA CURRENT APPLICATION NUMBER: US/10/981,293 CURRENT FILING DATE: 2004-11-04 PRIOR APPLICATION NUMBER: US/09/934,900
                              LENGTH: 92
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Cahoo
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Yadav, Naren
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Hitz, William
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. 6.3e-15;
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              ELVISLIVES PCR primer
                                                                                                                                                                                                        IN REDUCING
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                                                                                                                                                                                                          GENE EXPRESSION
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Sequence 24, Application US/09887194A
Publication No. US20030036197A1
GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
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US-09-887-194A-14/c
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                                                NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
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SEQ ID NO 14
LENGTH: 92
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Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
                                                                                                  FILE REFERENCE: BB1449 US NA CURRENT APPLICATION NUMBER: US/09/887,194A CURRENT FILING DATE: 2002-03-13
                                                                                                                                                  APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                 ENGTH:
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Pred. No.
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Pred. No.
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6.2e-15;
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                                                                                                                                                     THEIR USE IN REDUCING GENE EXPRESSION
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GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott B.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REPLE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-277
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US-10-389-647-277
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: region of pB568
US-09-887-194A-24
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; OTHER INFORMATION:
US-09-887-194A-24
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                                                    SEQ ID NO 277
LENGTH: 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 24
LENGTH: 1717
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                     Sequence 277, A Publication No.
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                                                                                                             PRIOR APPLICATION NUMBER: 60/153022
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 AGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 117
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                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                         Application US/10389647 o. US20040033549A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description of Artificial Sequence: region of pBS68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45.8; DB 10;
Pred. No. 0.00013;
0; Mismatches 2;
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Pred. No. 0.
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US-10-156-761-6327
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US-10-389-647-277/c
US-10-389-647-277/c
; Sequence 277, Application US/10389647
; Publication No. US20040033549A1
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                                                      APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FULE REFERENCE: 249-262
FURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2010-08-02
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Best Local S
Matches 61
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6327
LENGTH: 1581
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6327, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: QUORUM SENSING SIGNALING
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
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NUMBER OF SEQ ID NOS: 710
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APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
                                                                                                                                                                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/153022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1251
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
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Pred. No. 0.026;
D; Mismatches
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; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROS
; APPLICANT: SHIBA, TADAYOSH
                                                                                                                                US-10-156-761-1
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; LOCATION: (1)..(1581)
US-10-156-761-6327
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; LOCATION: (1)..(1581)
US-10-156-761-6327
                                                                                                                                               RESULT 37
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                                                                                              Sequence 1, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6327, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 15109
EQ ID NO 6327
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Streptomyces avermitilis FEATURE:
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                                                                                                                                                                                                                                                            417 CCCGAGCAGTTCGCCGGGCTCGTCCGGGCGTCGCAGTACGGAGGCGACGACCTCGCGGTT 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 TGACCAGCTCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGG 151
                                                                                                                                                                                                                             64 CGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCG 113
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                                                                                                                                                                                                                                                                                          4 CCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                                                                                                                                                               CGACGGGCCGTCGGTCACGCCCGCGTCGAGGCGCGCCTTGACGTACTCGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGTCGCCTCCGTACTGCGACGCCCGGACGACCCGGCGAACTGCTCGGG 417
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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59.1%;
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59.1%;
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Pred. No. 0.
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US-10-156-761-1/c
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                                              Query Match
                                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10156761 Publication No. US20030119018A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKKKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 249-262
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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                                                                                                                                      OTHER INFORMATION: a,
                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (4187715)
                                                                                                                                                                                            ORGANISM: Streptomyces FEATURE:
                                                                                                                                                                                                                                   TYPE: DNA
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LOCATION: (4187715)
OTHER INFORMATION: a, t,
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CCGGAGCTGGTCATCTCGCTCATCGTCGACGTCGGCGGAGCTGGTCATCTCGCTCAT
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HORIKAWA, HIROSHI
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                                            Conservative
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                                      Score 38; DB 15;
Pred. No. 0.018;
0; Mismatches 4
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Pred. No. 0.018;
0; Mismatches 45
                                                                           DB 15; Length 9025608;
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                                         NUMBER OF SEQ ID NOS:
SEQ ID NO 43250
LENGTH: 1821
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APPLICANT: La ROBA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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                                                                                                    APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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OTHER INFORMATION: Clone ID: PAT_MRT4530_46425C.1
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ORGANISM: Oryza sativa
                     TYPE: DNA
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Local Similarity 53.0%;
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Barbazuk, Brad
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Barbazuk, Brad
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                                                                                                                                                                         US-10-437-963-51952/c
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SEQ ID NO 51952
LENGTH: 742
                                                                                                                                          Sequence 51952, Application US/10437963
Publication No. US20040123343A1
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Publication No. US20040123343A1
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Best Local Similarity
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                                                                                             APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Wu, Wei
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Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
Li, Ping
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Zhou, Yihua
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Pred. No. 0.
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_8421C.1
US-10-437-963-85043
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_54296C:
US-10-437-963-51952
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LENGTH: 561
TYPE: DNA
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 51952
LENGTH: 742
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Publication No. US20040123343A1
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                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
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                                                                                      ATGACCAGCTCC 149
                                                                                                                                                 CCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGACTCGACTGAGCGAGGATGAGCGAG
                                                                                                                      CCGCCGCCGCCTCGCCACCCAAGACGACGGTCTCCGGCTACCGTCCCGATCACCATGACG
                                                   ACGACCACCACC 218
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Pred. No. 0
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US-10-437-963-85043/c

Indels

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
TYPE: DNA
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CURRENT APPLICATION UNMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
EQ ID NO 85043
LENGTH: 561
TYPE: DNP
                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_40691C.1 US-10-437-963-36912
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US-10-437-963-36912
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              Query Match
Best Local Similarity
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Publication No. US20040123343A1
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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ORGANISM: Oryza sativa
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Sear Job	Db	Ş	망	Ş	밁	Ş
Search completed: April 9, 2005, 01:03:46 Job time : 528 secs	538 GCCG 541	/ 151 GCCG 154	478 CACCACCACCACCAGCAGCGCGCCGCCGCCACCTCCGGCACCACTACTCAGCCCC 537	91 GATGAGCGAGATGACCAGCTCCGGCCGCCGACTGAGCGATGAGCGAGATGACCAGCTCCG 150	418 GAGCGCGAGCACGGATCCGGCCTCCACCATGACCTCGTCGGCCGCCGCCGCCGCCAC 477	31 GAGTCGGCGGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACTCGAC 90

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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                            New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
                                                                                                                                                                                                                                     Glassman KF,
                                                                                                                                                                                                                                                                                          23-JUN-2000; 2000US-0213961P
                                                                                                                                                                                                                                                                                                              22-JUN-2001; 2001WO-US019962
                                                                                                              Claim 45; Page 37;
                                                                                                                                                                                                                                                           (DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                      Gordon-Kamm WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2X ELVISLIVES
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complement(119. .148)
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (82. .111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  product= "ELVISLIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                  product= "ELVISLIVES protein"
                                                                                                              77pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression; plasmid pKS133; ds
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ABX34289
ADJ44648
ADJ44648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementary repeat DNA.
                                                                                                                                                                                                                                       Kinney AJ,
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                                                                                                                                                                                                                                       Lowe K,
                                                                                                                                                                                                                                        Stecca KL;
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD29231 standard; DNA; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 154 BP;
New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmids
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                                                                                                                                                                                        Glassman KF,
Nichols SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant construct; gene expression;
                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001; 2001WO-US019962
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P-PSDB; AAE18333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                   2000US-0213961P
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                                                                                                                                                                                                                 Gordon-Kamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2X ELVISLIVES complementary repeat DNA
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HI-BRED INT INC.
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complement(119. .148)
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Pred. No. 2.7e-28;
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                                                                                                                                                                                                                     Kinney AJ,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                  Rice; diverged coil; transgenic
22-AUG-2000; 2000US-0226996P
                                                                                                                                                                                                                                                                                                                                                                             Plasmid pKS133
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                         22-AUG-2001; 2001WO-US026246
                                                                              WO200216565-A2
                                                                                                                                                                                                                                                                                               Unidentified
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c plant;
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                                                                                                                                /product= "ELVISLIVES complement(119. .148)
                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                   product= "ELVISLIVES
                                                                                                                                                                                                                          product= "ELVISLIVES protein"
                                                                                                                                                            tag=
                                                                                                                                                                       omplement(82. .111)
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                                                                                                                                                                                                                                                                                                                                  fatty acid desaturase; enzyme; cellular lipid;
gene mapping; immunisation; plasmid pKS133; gene;
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                                                                                                     "ELVISLIVES protein
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Pred. No. 2.7e-28;
Pred. No. 2.7e-28;
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                                                                                                                                           protein"
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RESULT 4
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KW oil; t
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Best Local
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limiting, to isolate cDNAs and genes encoding homologous proteins from
the same or other plant species and to create transgenic plants in which
the polypeptides are present at higher or lower levels than normal or in
cell types or developmental stages in which they are not normally found,
thus altering the level of mono-, poly- and unsaturated fatty acids in
those cells. They are useful as probes for genetic and physical gene
mapping and as markers, e.g. restriction fragment length polymorphism
(RFLP) markers. The peptides can be used to immunise animals to produce
antibodies specific for the peptides and proteins. The present sequence
is IX ELVUSLIVES complementary repeat region DNA found in plasmid pXS133
This sequence is used in the exemplification of the invention for the
suppression of Pad2 in soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD32908
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                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                                                                                                                                                                              diverged delta-9 fatty acid desaturase; enzyme; cellular lip:
transgenic plant; gene mapping; immunisation; plasmid pKS133;
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Pred. No. 2.7e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to diverged delta-9 fatty acid desaturase components and polynucleorides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular clipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFILP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is 1X EIVISLIVES complementary repeat region DNA found in plasmid pKS133 This sequence is used in the exemplification of the invention for the
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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 23-SEP-2004
                                ADQ07968;
                                                           ADQ07968 standard; DNA; 154
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 154
                                                                                                                                                                                                                                                                                                                                                                                                                      suppression of Fad2 in soybean
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ilarity 100.0%;
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Pred. No. 2.7e-28;
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The invention relates to decreasing the ratio of liquiritigenin-derived isoflavones relative to the total isoflavones in an isoflavonoid-producing plant comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid sequence of at least 200 nucleotides having at least 75% sequence identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included are an isoflavonoid-producing plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product having a reduced ratio of liquirities form the plant of liquirities of the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Decreasing ratio of liquiritigenin-derived isoflavones relative to total isoflavones in a plant comprises transforming plant cell with nucleic acid sequence showing homology to sequence encoding chalcone reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dairy product; pet food product; animal feed; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pKS151; seed specific promoter; gene silencing; chalcone reductase; transgenic; liquiritigenin-derived isoflavone; isoflavonoid; transgenic; liquiritigenin-derived good product; fried food product; food product; baked good product; fried food product; health food product; infant formula; beverage; nutritional supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (deoxychalcone synthase).
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/*tag= a
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the total isoflavone levels obtained from the seeds or plant parts, a food (or a nutritional supplement, a food bar, or a beverage) which has incorporated the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels. The recombinant construct comprises to stem-loop structure. The nucleic acid sequence forms a loop in the stem-loop structure and the stem comprises a sequence of ADQ07968). The promoter is a seed-specific promoter. The method is useful for decreasing the ratio of liquiritigenin derived isoflavones relative to the total isoflavones in an isoflavone-producing plant. The methods and recombinant construct are useful in product, plant food product, snack food product which is incorporated in cereal food product, snack food product, baked good product, fried food product, health food product, infant formula, beverage, nutritional supplement, dairy product, pet food product, or animal feed. The present sequence is the single stranded version of the stem loop region from Sequence 154 BP; 24 A; 53 Ç 53 <u>Ģ</u> 24 T; 0 U; 0 Other; relative to

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Query Match

Local 154;

Similarity

100.0%; llarity 100.0%; Conservative (

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Score 154; DB 12; Pred. No. 2.7e-28; Mismatches 0;

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Gaps

60

CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT CEGCCEGAECTEGTCATCTCECTCATCETCGAETCGECEGCCGGAECTGGTCATCTCGCT

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RESULT AND OFFICE SECOND SECON
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                                                               The invention relates to decreasing the ratio of liquiritigenin-derived (C) isoflavones relative to the total isoflavones in an isoflavoned. CC producing plant comprising transforming a plant cell with a recombinant CC construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct producing a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct to ADQ07965 (a soybean chalcone reductase cDNA). Also included care an isoflavonoid-producing plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product converge a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels obtained from the seeds or plant parts, a food (or a nutritional supplement, a food bar, or a beverage) which has concorporated the isoflavonoid-containing product, and a method of corducing an isoflavonoid-containing product, and a method of corducing an isoflavonoid-containing product, and a method of corducing an isoflavonoid-containing product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone concleic acid sequence of ADQ07968). The promoter is a seed-specific promoter. The method is useful for decreasing the ratio of liquiritigenin concerving a lant The methods and recombinant construct are useful in an isoflavone.
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ADQ07968 standard; DNA; 154
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The invention relates to a plant comprising at least one recombinant DNA molecule comprising a promoter operably linked to at least a portion of at least one oxidosqualene cyclase gene, the molecule sufficient to suppress the production of a triterpene or any of its progeny, where the progeny comprise the molecule. The oxidosqualene cyclase gene catalyzes the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultiflorenol or any combination. The plants are useful in generating products which may be used as feeds, foods, beverages and industrial products like agricultural adjuvants, concrete supplies, dielectric fluids, dust suppressants, fuel additives, hydraulic fluids, industrial cleaners, industrial lubricants, metalworking fluids, odor reduction, paint
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic plants comprising recombinant DNA molecules encoding oxidosqualene cyclase to lower triterpene level, used as feeds, foo beverages and industrial products like agricultural adjuvants or co
                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 9; 39pp; English.
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                      The invention relates to a plant comprising at least one recombinant DNA molecule comprising a promoter operably linked to at least a portion of at least one oxidosqualene cyclase gene, the molecule sufficient to suppress the production of a triterpene or any of its progeny, where the progeny comprise the molecule. The oxidosqualene cyclase gene catalyzes the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin isomultiflorenol or any combination. The plants are useful in generating products which may be used as feeds, foods, beverages and industrial products like agricultural adjuvants, concrete supplies, dielectric fluids, dust suppressants, fuel additives, hydraulic fluids, industrial cleaners, industrial lubricants, metalworking fluids, odor reduction, paint
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Pred. No. 3.1e-28;
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or saw guide oils.
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Query Match

Sequence

7701

BP; 2236 A; 1702 C; 1709 G;

2053

Τ; 0

U; 1 Other;

Best Local Similarity

100.0%;

Score 154; DB 12; Pred. No. 3.1e-28;

Length 7701;

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RESULT 9
ADF6/892
ID 67/892
ID 70 ADF6
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XX Seed
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PF 12-1
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                                                       The invention relates to a method for increasing isoflavonoid production in a plant, by transforming the plant with a recombinant DNA construct having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone 3-hydroxylase, and second recombinant DNA construct having a PN encoding Cl myb and a R myc-type transcription factor, growing the transformed plant, and evaluating the quantity of isoflavonoid from the plant. The method of the invention is useful for increasing isoflavonoid production in an isoflavonoid-producing plant. The current sequence represents the seed-specific expression vector pKS151, into which a polynucleotide encoding a portion of soybean flavanone 3-hydroxylase was inserted in an example from the invention, for the transformation of Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               may play a defense role against pathogens in plant tissues. The present sequence represents the nucleotide sequence of a seed-specific expression vector pKS151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing isoflavonoid production in an isoflavonoid-producing plant, comprises transforming a plant with recombinant DNA constructs, growing the transformed plant, and evaluating increased quantity of isoflavonoid.
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RESULT 10
ADP67892/c
ID ADP67892 standard; DNA; 7701 BP
XX
ADP67892;
XX
AC ADP67892;
XX
DT 11-MAR-2004 (first entry)
XX
Seed-specific expression vector
XX
Isoflavonoid; transgenic plant;
XX
OS Synthetic.
XX
OS Synthetic.
XX
PD 24-DEC-2003.
XX
PF 12-JUN-2003; 2003WO-US018663.
XX
PF 12-JUN-2002; 2002US-0388280P.
XX
PR 13-JUN-2002; 2002US-0388280P.
XX
PR 13-JUN-2002; 2002US-0388280P.
XX
PR 13-JUN-2002; 2002US-0388280P.
XX
PR 13-JUN-2003; 2003WO-US018663.
XX
PF 12-JUN-2003; 2003WO-US018663.
XX
PF 13-JUN-2003; 2003WO-US018663.
XX
PF 13-JUN-2003; 2003WO-US018663.
XX
PF 13-JUN-2003; 2003WO-US018663.
XX
PF 12-JUN-2003; 2003WO-US018663.
XX
PF 13-JUN-2003; 2003WO-US018663.
XX
PF 
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                                                                                                                                                                                                                                Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for increasing isoflavonoid production in a plant, by transforming the plant with a recombinant DNA construct having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone 3-hydroxylase, and second recombinant DNA construct having a PN encoding C1 myb and a R myc-type transcription factor, growing the transformed plant, and evaluating the quantity of isoflavonoid from the plant. The method of the invention is useful for increasing isoflavonoid production in an isoflavonoid-producing plant. The current sequence represents the seed-specific expression vector pKS151, into which a polynucleotide encoding a portion of soybean flavanone 3-hydroxylase was inserted in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing isoflavonoid production in an isoflavonoid-producing plant, comprises transforming a plant with recombinant DNA constructs, growing the transformed plant, and evaluating increased quantity of isoflavonoid
                                                                                                                                                                                                                                                                                                                       Sequence 7701 BP; 2236 A; 1702 C; 1709 G;
                                                                                            5604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5571
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                                                                                                                                                                                                           154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154;
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DU PONT DE NEMOURS & CO
CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
                                                                                         CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
                                                                                                                          CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCCGGAGCTGGTCATCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 5604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1; 55pp; English.
                                                                                                                                                                                                     100.0%;
ilarity ,100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression vector pKS151 #SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                             for the transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                  Score 154; DB 12;
Pred. No. 3.1e-28;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         flavanone 3-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                       2053
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                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                             ase was inserted of Glycine max.
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                                                                                                                                                                                                                                                                                                                       U; 1
                                                                                                                                                                                                                                                           7701;
                                                                                                                                                                                                                                                                                                                       Other;
                                                                                                                                                                                                     0;
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                                                                                      5545
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                                120
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RESULT 11
ADQ07962
ADQ077
XX ADQ07
XX ADQ07
XX ADQ07
XX ADQ07
XX ADQ07
XX ADQ07
XX Seed
XX PXS15
XX Frich
XX Glyci
OS Egchei
OS Hachei
OS Glyci
OS Egchei
OS Glyci
OS Egchei
OS Glyci
OS Hachei
OS Glyci
OS Egchei
OS Egchei
OS Egchei
OS FT CDS

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plant parts of the plant, an isoflavonoid-containing protein product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels obtained from the seeds or plant parts, a food (or a nutritional supplement, a food bar, or a beverage) which has incorporated the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels. The recombinant construct comprises a stem-loop structure and the nucleic acid sequence forms a loop in the stem-loop structure and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max.
Escherichia d
Cauliflower n
                                                                                                                                                                                                                                                                                            The invention relates to decreasing the ratio of liquiritigenin-derived isoflavones relative to the total isoflavones in an isoflavonoid-producing plant comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid sequence of at least 200 nucleotides having at least 75% sequence identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included are an isoflavonoid-producing plant made by the method above, seeds or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Decreasing ratio of liquiritigenin-derived isoflavones relative to total isoflavones in a plant comprises transforming plant cell with nucleic acid sequence showing homology to sequence encoding chalcone reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2002; 2002US-0433433P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic; liquiritigenin-derived isoflavone; plant; soybean; isoflavonoid; food product; snack food product; baked good product; fried food product; infant formula; beverage; nutritional supplement; dairy product; pet food product; animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 1; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2003; 2003US-00734947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pKS151; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MCGO/) MCGONIGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (deoxychalcone synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-533136/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ07969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coli.
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/note= "No start or stop codon
/product= "ELVISLIVES peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene silencing; chalcone reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shown"
                                                                                                                                                                                                                                      relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb
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stem comprises a sequence of ADQ07968). The promoter is a seed-specific promoter. The method is useful for decreasing the ratio of liquiritigenin derived isoflavones relative to the total isoflavones in an isoflavone-producing plant. The methods and recombinant construct are useful in producing an isoflavonoid-containing product which is incorporated in cereal food product, snack food product, baked good product, fried food product, health food product, infant formula, beverage, nutritional supplement, dairy product, pet food product, or animal feed. The present sequence is the Seed specific gene silencing vector pKS151, into which the soybean cDNA is cloned (into the NotI site flanked by the stem

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RABSULT 12
ADQ07962/G
ID ADQ079
XX ADQ079
XX ADQ079
XX Eseed s
XX Eseed s
XX PXS151
KW transg
KW transg
KW fried
KW transg
KW fried
KW fried
KW fried
KW fried
KW fried
KW fried
KW Schried
KW fried
KW Schried
KW Schried
KW Transg
KW 1sofia
KW Glycin
OS Escher
OS Caulife
XX Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pKS151; seed specific promoter; gene silencing; chalcone reductase; transgenic; liquiritigenin-derived isoflavone; plant; soybean; isoflavonoid; food product; snack food product; baked good product;
   WPI; 2004-533136/51.
P-PSDB; ADQ07969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Cauliflower mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoflavonoid; food product; snack food product; baked good product; fried food product; health food product; infant formula; beverage; nutritional supplement; dairy product; pet food product; animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seed specific gene silencing vector pKS151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ07962 standard; DNA; 7701
                                                                                                                                                                                                                                                                                                                             11-DEC-2003; 2003US-00734947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004128714-A1.
                                                                                                        Mcgonigle
                                                                                                                                                                                                                                                      13-DEC-2002; 2002US-0433433P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5571
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                                                                                                                                                                                      MCGONIGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5457. .5486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "No start or stop codon shown"
/product= "ELVISLIVES peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 partial/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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Decreasing ratio of liquiritigenin-derived isoflavones relative to toti isoflavones in a plant comprises transforming plant cell with nucleic acid sequence showing homology to sequence encoding chalcone reductase (deoxychalcone synthase). total

Example 1; SEQ ID NO 1; 25pp; English.

CC producing plant comprising transforming a plant cell with a recombinant CC producing plant comprising transforming a plant cell with a recombinant CC construct comprising a promoter operably linked to a nucleic acid CC cidentity to ADD07965 (a soybean chalcone reductase CDNA). Also included are an isoflavonoid-producing plant made by the method above, seeds or CC plant parts of the plant, an isoflavonoid-containing protein product CC thaving a reduced rattio of liquiritigenin-derived isoflavones relative to the total isoflavone levels obtained from the seeds or plant parts, a food (or a nutritional supplement, a food bar, or a beverage) which has incorporated the isoflavonoid-containing product, and a method of CC promoters an isoflavonoid-containing product, and a method of CC quirititigenin-derived isoflavones relative to the total isoflavone (CC promoter. The recombinant construct comprises a stem-loop structure. The comprises a sequence forms a loop in the stem-loop structure and the containing product. The producing plant. The method is useful for decreasing the ratio of liquiritigenin cereal food product, snack food product, baked good product, firled food product, health food product, infant formula, beverage, nutritional comproduct and isoflavone-present sequence is the Seed specific gene silencing vector pXS151, into which the stem objects of the soybean cDNA is cloned (into the NotI site flanked by the stem The invention relaties to decreasing the ratio of liquiritigenin-derived isoflavones relative to the total isoflavones in an isoflavonoidregions of ADQ07968.

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5

CATCGTCGAGTCGGCCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 

5451

Matches 154; Conservative

Similarity

100.0%;

Score 154; DB 12; Pred. No. 3.1e-28; ; Mismatches 0;

Indels Length u; 1

<u>.</u>

Gaps

0

5510 120

60

7701; Other;

0;

1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT

Query Match Best Local :

Sequence 7701 BP; 2236 A; 1702 C; 1709 G;

2053 H; 0 of ADQ07968.

Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

밁 Ş 밁 8 밁 Ş Query Match Best Local & Matches Local 5484 5544 5604 154; 61 Н Similarity CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 100.0%; ilarity 100.0%; Conservative 0 0; Score 154; Pred. No. 3 Mismatches 3.1e-28; DB 12; 5451 154 Indels Length 7701; 0 Gaps 120 5545 60 5485 0

RESULT 13 ABK10072 ABK10072; ABK10072 standard; DNA; 4974 ΒP

Plasmid pKS133 DNA 05-JUN-2002 (first entry)

Synthetic Plastidic phosphoglucomutase; gene; ds; plasmid pKS133

EP1174510-A2

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RESULT 14
ABK10072/c
ID ABK100
XX
AC ABK100
XC
AC ABK100
DT 05-JUN
XX
DE Plasmi
XX
Plasti
XX
OS Synthe
XX
PD EP1174
XX
PD 23-JAN
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC Polynucleotide fragments are useful for suppressing the level of CC expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the CC phosphoglucomutase activity. An isolated polynucleotide that affects the CC least of expression of a plastidic phosphoglucomutase polypeptide in a CC least 541 nucleotides, measuring the level of the polypeptide in the CC plant cell containing the polynucleotide, and comparing the level of the polypeptide in the CC the level of the plant cell containing the isolated polynucleotide with CC the level of the polypeptide in a plant cell that does not contain the CC isolated polynucleotide. A method for altering the level of expression of CC a plastidic phosphoglucomutase protein in a host cell comprises CC isolated polynucleotide. A method for altering the level of expression of CC cell under conditions that are suitable for expression of the chimeric CC gene, where the expression of the gene results in production of altered CC levels of plastidic phosphoglucomutase. This sequence represents plasmid CC levels of plastidic phosphoglucomutase. This sequence is not represented in the printed specification but is based on sequence is not of conformation supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                         23-JAN-2002
                                                               EP1174510-A2
                                                                                                      Synthetic
                                                                                                                                          Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
                                                                                                                                                                                                                             05-JUN-2002
                                                                                                                                                                                                                                                                        ABK10072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; SEQ ID NO 17; 27pp; English
                                                                                                                                                                                  Plasmid pKS133 DNA.
                                                                                                                                                                                                                                                                                                            ABK10072 standard; DNA; 4974
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                CATCGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCC 4974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001EP-00306143
                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.7%; Score 112; DB 6;
100.0%; Pred. No. 4.5e-18
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carlson TJ, Ilag LL;
                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5e-18;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
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DX SX FX GX GX SX E FF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to plastidic phosphoglucomutase polypeptides and cc transgenic plant, by transforming a plant cell with a polypucleotide of the invention and regenerating a plant from the transformed plant cell. CC Polynucleotide fragments are useful for suppressing the level of cc expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the cc level of expression of a plastidic phosphoglucomutase polypeptide in a cc plant cell can be identified by introducing a DNA fragment comprising at cc plant cell containing the polynucleotide, and comparing the level of the polypeptide in the cc plant cell containing the polynucleotide, and comparing the level of the polypeptide in a plant cell that does not contain the cc isolated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises cc ransforming a host cell with a chimeric gene and growing the transformed cc levels of plastidic phosphoglucomutase. This sequence represents plasmid CC levels of plastidic phosphoglucomutase. This sequence is not cc represented in the printed specification but is based on sequence is not conformation supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                      oil; transgenic
                                                                                                                        Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
                                                                                                                                                         pBS68 plasmid used for diverged delta-9 desaturase suppression
                                                                                                                                                                                             01-JUL-2002
                                                                                                                                                                                                                                                              AAD32909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-156692/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-2000; 2000US-0218712P
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                                                                                                                                                                                                                                                                                                                                                                                                                       4974
                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
112; Conserv
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                                                                                                                                                                                                                                                            standard; DNA; 6611
                                                                                                                                                                                                                                                                                                                                                    GACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                        GACCAGCTCCGGCCGACCTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGACTCTCGACGATGAGCGAGAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Butler KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           (first entry)
Location/Qualifiers 523. .725 /*tag= b
                                                                                                    plant; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                        immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.5e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                        plasmid pBS68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                      4863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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terminator

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RESULT 16
AAD32909/c
ID AAD32909 standard; DNA; 6611 BI
XX
AC AAD32909;
XX
DT 01-JUL-2002 (first entry)
XX
DT pBS68 plasmid used for diverged
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                         thus altering the level of mono, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFIP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is plasmid pB868 which is used for the suppression of diverged delta-9 desaturase in high stearate phenotypes. This sequence is used in the exemplification of the invention. Note: The sequence data for this sequence (AAD32909) corresponding to position 1501 to 6611 is not represented in the printed specification but is based on the sequence information supplied by the European patent office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lover levels than normal or in coll transpositions.
 pBS68 plasmid used for diverged delta-9 desaturase suppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, po and unsaturated fatty acids and in increasing the unsaturation levels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6611 BP; 1831 A; 1472 C; 1453 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell types or developmental stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in cellular lipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Booth JR,
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                                                                                                                                                                                                 5408
                                                                                                                                                                                                                                                                       5348
                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Page 76-77; 77pp; English
                                                                                                                                                                                                                                                                                             CATCGTCGAGTCGGCGGCCGCTGAGT 5433
                                                                                                                                                                                                                     CATCGTCGAGTCGGCGGCCGCCGACT
                                                                                                                                                                                                                                                                       CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 5407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Kit3_terminator
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97.7%;
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                                                                                                                                                                                                                                                                                                                                    Score 82.8; DB b;
Pred. No. 5.4e-11;
                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in which they are not normally found,
                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                             1854 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yadav NS
                                                                                                                                                                                                                                                                                                                                                                         Length 6611;
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CC proteins and polynucleotides encoding such proteins. The nucleic acid CC sequences may be used to increase the level of unsaturation in cellular CI lipids, including oil, in tissues when the enzyme is absent or rate-cc limiting, to isolate cDNAs and genes encoding homologous proteins from CC the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in CC cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in CC those cells. They are useful as probes for genetic and physical gene CC (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is plasmid pBS68 which is used for the suppression of diverged delta-9 ce semplification of the invention. Note: The sequence is used in the exemplification of the invention. Note: The sequence data for this sequence (AAD32909) corresponding to position 1501 to 6611 is not represented in the printed specification but is based on the sequence information supplied by the European patent office
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly and unsaturated fatty acids and in increasing the unsaturation levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 76-77; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-2000; 2000US-0226996P
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                                                                                                                                                                                                                                                       Local Similarity
5373
                                                                                                              5433
                                                  129
                                                                                                                                                                    69
                                                                                                                                                                                                                            84;
                                                                                                                                                                                                                                                                                                                                           6611
                                                                                                                                                        AGTCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
                                                     ATGAGCGAGATGACCAGCTCCGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to diverged delta-9 fatty acid desaturase
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                           BP; 1831 A; 1472 C; 1453 G; 1854 T;
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3260. .5348
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                                                                                                                                                                                                                                                       53.8%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitz WD,
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Pred. No. 5.
                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                  DB 6;
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RESULT 17
ABK10711
                                        level of expression of a plastidic phosphoglucomutate polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polypeptide, and comparing the level of the polypeptide in the plant cell containing the isolated polynucleotide with the level of the polypeptide in a plant cell that does not contain the isolated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Artificial DNA sequence #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2002
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                                                                                                                                                                                                                                                        Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the
                                                                                                                                                                                                                                                                                                                                                                                            Example
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DB; AAU77109.
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/partial
/note= "No start or stop codon shown"
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Query Match

52.6%;

Score 81;

BB 6;

Length 81;

Sequence 81

BP; 8

A; 28 C; 29 G; 16 T; 0 U; 0 Other;

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RESULT 18
ABK10711/c
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The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide in a plant cell that does not contain the
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DB; AAU77109.
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                                                                                                                                                                                                                                                                                                                              Page 19; 27pp;
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/note= "
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RESULT 19
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construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glassman
Nichols S
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO )
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                                                                                                                                                                                                                                                                                                         The present invention relates to a new recombinant
                                                                                                                                                                                                                                                                                                                                                                    Example 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2000; 2000US-0213961P
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PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                 72; 77pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
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Pred. No.
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Best Local
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Nichols SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant construct; gene expression; late-soybean-embryo LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
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PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 243 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complementary region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       td
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter;
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least on target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived it. The present sequence is 2X ELVISLIVES complementary region from New recombinant construct having a promoter operably linked to sequence which when expressed produces an RNA having homology t mRNA and its reverse complement unrelated to endogenous DNA, fo Example 10; expression. Page 72; 77pp; English. for to a target

from

WPI; 2002-139927/18.

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DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBS149 that contains fragments from two soybean galactinol synthase genes GAS1 and GAS2. The region is functionally attached to a late-soybean-embryo promoter (LEA) and a phaseolin 3' terminator region. This entire region is then cloned into BamHI site of pKS136, which contains a 2X ELVISLIVES complementary region controlled by a soybean Kti promoter and terminator region used in the exemplification of the invention
                                                                                             New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a tament and its reverse complement unrelated to endogenous DNA, for red
                                                                                                                                                                              Glassman KF,
Nichols SE;
                                                                                                                                                                                                                                                    23-JUN-2000; 2000US-0213961P
                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-US019962
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 963
            when expressed by a
                                    The present invention relates to a new recombinant construct.
                                                             Claim 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant
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                                                                                                                                                                                                                  (PION-)
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                                                                                                                                             2002-139927/18.
DB; AAE18333.
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PIONEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCGTCGAGTCGGCGGCCGC 81
                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 240 A; 243 C; 248 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                           Gordon-Kamm WJ,
                                                             37;
                                                                                                                                                                                                                 HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                        complement (45.
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               product= "ELVISLIVES protein"
                                                                                                                                                                                                                                                                                                                                                                                   product=
                                                           77pp;
             a promoter operably host produces an RNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 81; 100.0%; Pred. No.
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omoter operably linked to a DNA sequence which produces an RNA having homology to at least or the host and complementary PNA roginary
                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                   "ELVISLIVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression; plasmid pKS124; plasmid pKS106;
                                                                                                                                                                                           Kinney
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                                                                                                                                                                                                                                                                                                                                                                                  protein"
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                                                                                                                                                                                           Lowe
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Claim 45; Page 37;

77pp; English

New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing gene expression.

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RESULT 22
AAD29230/c
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Best Local
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                                                                                                                Glassman
                                                                                                                                                                                                                                                                                             CDS
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                                                                           WPI; 2002-139927/18.
P-PSDB; AAE18333.
                                                                                                                                   (DUPO )
                                                                                                                                                                23-JUN-2000; 2000US-0213961P.
                                                                                                                                                                                                      03-JAN-2002.
                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                        Plasmids pKS106,
                                                                                                                                                                                                                                                                                                                                                                                                              AAD29230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                        Nichols
                                                                                                                                                                                   22-JUN-2001; 2001WO-US019962
                                                                                                                                                                                                                          WO200200904-A2.
                                                                                                                                                                                                                                                                                                                                                      Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 1X ELVISLIVES complementary repeat region leading in plasmids pKS106 and pKS124 used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
                                                                                                       n KF,
SE;
                                                                                                                                   DU PONT DE NEMOURS & CO
PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGACTCGACGATGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      construct; gene expression; plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                Gordon-Kamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                               complement (45.
                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                            /product=
                                                                                                                                                                                                                                                               /product= "ELVISLIVES complement(45. .74)
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        pKS124 1X ELVISLIVES complementary repeat DNA
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                                                                                                                                                                                                                                             "ELVISLIVES
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Pred. No.
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                                                                                                                 Kinney
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Matches 80
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                          New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly - and unsaturated fatty acids and in increasing the unsaturation levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pKS124;
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                                                                                                                                                                                                                                                        Booth JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                       (DUPO)
                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2001; 2001WO-US026246
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cellular lipids
                                                                                                                                                           2002-269353/31.
DB; AAE20554.
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                                                                                                                                                                                                                                                                                                                       DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pKS106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGATGACCAGCTCCGGCCG 117
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                                                                                                                                                                                                                                                        Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      2000US-0226996P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (45. .74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pKS124 1X ELVISLIVES complementary repeat DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "ELVISLIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "ELVISLIVES protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 C;
                                                                                                                                                                                                                                                        Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 G;
                                                                                                                                                                                                                                                        Kinney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Le
2.2e-10;
                                                                                                                                                                                                                                                           ΑJ,
                                                                                                                                                                                                                                                              Yadav NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is 1X ELVISILVES complementary repeat region DNA found in plasmids pKS106 and pKS124. This sequence is used in the exemplification of the invention for the suppression of Fad2 in soybean
Sequence 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-lipids, to isolate CDNAs and genes encoding homologous proteins from the contract of the contract of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 43; 77pp; English.
BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
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RESULT 24
AAD32907/c
ID AAD329
XX AAD329
XX Plasmi
XX Plasmi
XX Plasmi
XX Uniden
XX CDS
FT CDS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pKS124; plasmid pKS106; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD32907 standard; DNA;
         P-PSDB; AAE20554
                                    WPI; 2002-269353/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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                                                                                             Booth JR, Cahoon RE,
                                                                                                                                                                                                               22-AUG-2000; 2000US-0226996P
                                                                                                                                                                                                                                                                     22-AUG-2001; 2001WO-US026246
                                                                                                                                                                                                                                                                                                                                 28-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
                                                                                                                                                         (DUPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (45. .74)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                product= "ELVISLIVES protein"
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                                                                                                                                                         NEMOURS & CO
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                                                                                             Hitz WD,
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Pred. No.
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                                                                                                Kinney AJ,
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. 2.2e-10;
                                                                                                Yadav NS
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Example 9; Page 19; 27pp;

English.

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RESULT 25
ABK10712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC proteins and polynucleotides encoding such proteins. The nucleic acid CC sequences may be used to increase the level of unsaturation in cellular CC lipids, including oil, in tissues when the enzyme is absent or rate-cC limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which CC the same or other plant species and to create transgenic plants in which CC they competides are present at higher or lower levels than normal or in CC thus altering the level of mono-, poly- and unsaturated fatty acids in CC those cells. They are useful as probes for genetic and physical gene CC mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce is 1X ELVISLIVES complementary repeat region DNA found in plasmids pXS106 and pXS124. This sequence is used in the exemplification of the invention CC for the suppression of Fad2 in soybean
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Best Local S
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            Novel isolated polypeptides having phosphoglucomutase activity and polynuclectides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein levels.
                                                                                          WPI; 2002-156692/21
                                                                                                                                                                                  17-JUL-2000; 2000US-0218712P.
                                                                                                                                                                                                                 17-JUL-2001;
                                                                                                                                                                                                                                                 23-JAN-2002.
                                                                                                                                                                                                                                                                                EP1174510-A2
                                                                                                                                                                                                                                                                                                                                         Plastidic phosphoglucomutase; transgenic; plant; gene;
                                                                                                                                                                                                                                                                                                                                                                         Artificial DNA sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK10712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK10712 standard; DNA; 92 BP
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                                                                                                                                                      ( ogud)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention relates to diverged delta-9
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                                                                                                                      Butler KH,
                                                                                                                                                      PONT DE NEMOURS & CO E
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100.0%; Pr
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                                                                                                                       Carlson
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2.2e-10;
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                             protein
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leic acid
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RESULT 26
ABKL0712/c
ID ABKL077
XX ABKL077
XX ABKL07
XX D5-JUN
XX Plasti
XX Plasti
XX Plasti
XX Plasti
XX 23-JAN
XX 23-JAN
XX 17-JUL
XX AUPO
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PT POlynu
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PS Exampl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transferning a plant cell with a polymucleotide of the invention and regenerating a plant from the transformed plant cell. CC Polymucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polymucleotide that affects the cc phosphoglucomutase activity. An isolated polymucleotide that affects the clavel of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at compart cell can be identified by introducing a DNA fragment comprising at plant cell containing the level of the polypeptide in the plant cell containing the isolated polymucleotide with the collected polymucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed cc cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered clevels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                   Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to plastidic phosphoglucomutase polypeptides an their related nucleic acids. The sequences are seful for producing a transgenic plant, by transforming a plant cell with a polynucleotide the invention and regenerating a plant from the transformed plant cel
                                                                                                                                                                                                                          17-JUL-2000; 2000US-0218712F
                                                                                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                               EP1174510-A2
                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                Plastidic phosphoglucomutase; transgenic; plant; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                    Artificial DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 92 BP; 16
                                                                                                                       WPI; 2002-156692/21.
                                                                                                                                                                                                                                                            17-JUL-2001; 2001EP-00306143
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Example

9; Page 19; 27pp; English

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RESULT 27
AAD29232
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CC invention

CC invention

CC invention
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Best Local :
New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing gene expression.
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PIONEER HI-BRED INT INC.
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target

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RESULT 28
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                                                                                                                                                                                                                                                 New recombinant construct having a promoter operably linked to a sequence which when expressed produces an RNA having homology to mRNA and its reverse complement unrelated to endogenous DNA, for
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Nichols SE;
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                                                                                                                                                                     Example 7;
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from
                                                                                                                                                                                                                                                   New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
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Nichols SE;
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PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                      Page 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 16 A;
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desaturase; plasmid pBS68; ds.
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                                                                                                                                                                                                      English.
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Pred. No.
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Best Local Similarity
                                                                          construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from pBS68 which contains 2X ELVISIIVES complementary regions surrounding the the nucleotide Fad2-1 NotI fragment from pKS11 and a nucleotide fragment from a soybean delta-9 desaturase gene used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                it. The present sequence is an analysis complementary regions surrounding the which contains 2X ELVISLIVES complementary regions surrounding the nucleotide Fad2-1 NotI fragment from pKS111 and a nucleotide fragment from a soybean delta-9 desaturase gene used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a tamRNA and its reverse complement unrelated to endogenous DNA, for red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glassman KF,
Nichols SE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new recombinant construct. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 70;
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ta-9 desaturase; plasmid pBS
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or reducing
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Best Local Similarity
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                                                                                             The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide in a plant cell of the polypeptide in a plant cell that does not contain the isolated polynucleotide. A method for altering the level of expression of a plant cell that does not contain the isolated polynucleotide. A method for altering the level of expression of
a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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                           The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a cransgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide in the polypeptide in the polypeptide in the polypeptide in the polypeptide. A method for altering the level of contain the containing the level of the polypeptide. A method for altering the level of contain the containing the level of a plastidic phosphoglucomutase protein in a host cell comprises that the containing the level of the polypeptide in the plant cell with a chimeric gene and growing the transformed that the containing the level of the polypeptide that a plant cell comprises that the containing the level of the polypeptide that the containing the level of the polypeptide in the plant cell with a chimeric gene and growing the transformed that the containing the level of the polypeptide that a chimeric gene and growing the transformed that the containing the level of the polypeptide that a chimeric gene and growing the transformed that the chimeric gene and growing the transformed that the chimeric gene and growing the transformed that the containing the level of the polypeptide that the chimeric gene and growing the transformed that the chimeric gene and growing the transformed that the chimeric gene and growing the transformed that the containing the level of the polypeptide that the chimeric gene and growing the polypeptide that t
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ith a chimeric gene and growing are suitable for expression of
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                                                                                                                                                                                        The present invention relates to a method for identifying a modulator of quorum sensing signalling in bacteria. The method comprises: providing a cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798), where the cell is responsive to a quorum sensing signal molecule such that a detectable signal is generated; contacting the cell with a quorum sensing signal molecule in the presence and absence of a test compound; and detecting a change in the detectable signal. The method and modulator identified by the method are useful for treating a biofilm-associated disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections, acne, periodontal disease, catheter-associated infections, and medical device-associated infections. Note: The sequence data for this patent was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quorum sensing signalling; bacterium; quorum sensing controlled gene; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; acne; periodontal disease; gene; ds; PA4304.
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                                                                                                                  Sequence 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 277; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with a quorum sensing signal molecule in the presence and absence test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a modulator of quorum sensing signaling in bacteria, usef for treating a biofilm-associated disorder, comprises contacting the
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                             Score 38.2;
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                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            The present invention relates to a method for identifying a modulator of quorum sensing signalling in bacteria. The method comprises: providing a cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798), where the cell is responsive to a quorum sensing signal molecule such that a detectable signal is generated; contacting the cell with a quorum sensing signal molecule in the presence and absence of a test compound; and detecting a change in the detectable signal. The method and modulator identified by the method are useful for treating a biofilm-associated disease or disorder, e.g. cystic fibrosis, ADIS, middle ear infections, acne, periodontal disease, catheter-associated infections, and medical device-associated infections. Note: The sequence data for this patent was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                 Sequence 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenberg EP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a modulator of quorum sensing signaling in bacteria, usef
for treating a biofilm-associated disorder, comprises contacting the
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Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral; antifungal sugar beet;

Eukaryota

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US2004016025-A1.
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26-SEP-2002; 2002US-00260238

26-SEP-2001; 26-SEP-2001; 04-APR-2002; (MOUG/) BUDWORTH P. MOUGHAMER T. 2001US-0325277P. 2001US-0325448P. 2002US-0370620P.

(BRIG/) (COOP/) (GLAZ/) (GOFF/) (KATA/) KREP KREPS J. PROVART N. GOFF S GLAZEBROOK J. GOFF S A. KATAGIRI F.

BRIGGS S P. COOPER B.

(ZHUT/) PROV/) RICKE D. ZHU T.

Budworth Goff SA, P, Moughamer Katagiri F, T, Br Kreps Briggs ps J, P Provart N, r B, ( Glazebrook J; e D, Zhu T;

WPI; 2004-190374/18

New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities or proteins, resistance to insecticides, virus or fungi, stress to proteins, resista value. tolerance of oil

Claim 25; QES ID NO 1055; 230pp; English

leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stransc to generate to alter or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this invention relates to plant nucleotide sequences that direct seed-

Claim

25; SEQ

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NO 1055; 230pp; English.

rne invention relates to plant nucleotide sequences that leaf- and/or stem-, panicle-, root- or pollen-specific or

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direct irect seed-, -preferential

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26-SEP-2001;
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                                                                                                        New rice promoter, useful for manipulating crop plants to improve phenotypic characteristics, e.g. produce large quor proteins, resistance to insecticides, virus or fungior high nutritional value.
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Pred. No. 1
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                                                                                                                                                                                                                                                             Cooper B, (
rt N, Ricke
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e D, Zhu T;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynuclectides and the polypeptides they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                  New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                            (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                  SEQ ID NO 24874; 80pp; English
                                                                                                                                                                                                                          Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived single exon probe #24874.
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; Pred. No. 18;
0; Mismatches
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expression, co

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and

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RESULT 38
ACH91679/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc encoding at least 8 amino acids of any of the 6888 amino acid sequences chilly defined in the specification. The probe is a single exon probe that cc hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-cc addressable set of single exon nucleic acid probes for measuring human comprising a plurality of single exon nucleic acid probes is separately combes cited above, where each of the plurality of probes is separately cand addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of contiguous amino acids of any of the above mentioned amino acid sequences (optionally with conservative amino acid substitutions), an cc isolated antibody that binds specifically to a peptide cited above, an oRF-encoded peptide comprising at least 8 cmethods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing thuman gene expression data by subscription, and a computer-readable exon grapes endium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene contains the probes may be used as tools for surveying creations in the genomic locus that includes their exon, in assessing sallition, the probes are used in identifying and characterising gross calternative splicing events, in detecting and characterising cross calternative splicing the ORF-encoded peptide. The spresses of mucleic acids, or in expressing the ORF-encoded peptide. The sequence is a human considered in the probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained confidence in the command of the printed specification.
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Best Local Similarity
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                                                           03-APR-2002; 2002US-00029386
                                                                                                     03-APR-2002; 2002US-00029386
                                                                                                                                                                                         US2003194704-A1
                                                                                                                                                                                                                                                                                                                                       Human genome derived single exon probe #24874.
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(PENN/) PENN S
(RANK/) RANK D
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
PRO polypeptide encoding cDNA SEQ ID NO:1808
                                            18-NOV-2004
                                                                                                                     ADP24630 standard; cDNA; 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html?DocID=20030194704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 24874; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                      22.7%;
56.5%;
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                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 362
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              G;
                                                                                                                                                                                                                                                                                                                                                                                                                                              86 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          DВ
                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 850;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                      cc systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, colleged to the control of the control o
                                                                                                                                                                                                                                                                                                                    eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as
                                                                                                                                                                                                                                                       Sequence 1797
                                                                                                                                                                                                                                                                                                                                                                       eosinophilic pneumonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosup osteopathic, antidiabetic, dermatological, antipsoriatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated erenal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark H,
Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2002; 2002US-0423394P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-2003; 2003WO-US034312
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                                                             597
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            62
                                                                                                                                                           65;
                                                                                                           N
                                                                                                                                                                               Similarity
ATCGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
                                                                                 GGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP24631.
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                                                     SEQ ID NO 1808; 2940pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schoenfeld J,
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                       B₽;
                                                                                                                                                                                                                                                       263 A; 645
                                                                                                                                                                        22.7%;
56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological, antipsoriatic,
                                                                                                                                                      <u>,</u>
                                                                                                                                                   Score 35; DB Pred. No. 20; 0; Mismatches
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                                                                                                                                                                                                                                                    552 G;
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                                                                                                                                                                                               Length 1797;
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                                                                                                                                                                                                                                                  0 Other;
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                                                                                                                                                 Gaps
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GCCTCTGCGTGGGCTGCGGCTGGGTCGCCGCACTGGCCGCCTCCGGCC

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RESULT 40
ADP24630/c
                                                                                                                                                                              systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, a idiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, a resculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, an autoimmune or immune-mediated skin disease, a bullous skin
                                                                                                                     disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipporiatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, it agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as
                                                      eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-med renal disease, or demyelinating diseases of the central or periphe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated nucleic acid and the polypeptide encoded by it. A protein of the invention has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; osteopathic; antidiabetic; dermatological;
antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-419628/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2002; 2002US-0423394P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; antiarthritic; antirheumatic;
ive; osteopathic; antidiabetic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2940pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, its
                                                          protein of
                                                                                                                                                                                                                                                                                      syndrome
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Query Match Best Local Similarity

22.7**%**; 56.5**%**;

Score Pred.

35; No. DB 20;

13;

Length 1797

Sequence

B₽,

263

A; 645 C;

552 G;

337 T; 0 U; 0 Other;

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                                                                                                         Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                     The present invention relates to recombinant DNA vectors (cosmids) that encode for the narbonolide polyketide synthase (PKS) enzyme and various narbomycin modification enzymes from Streptomyces narbonensis. The recombinant DNA vectors can be used to produce recombinant ketide synthases and a variety of different polyketides (e.g. erythromycin, rapamycin, tylosin, narbomycin, picromycin, methylmycin and neomethymycin) for use in agriculture, medicine and health. The recombinant vectors may be used to produce polyketides in relatively high yields. AAS18432-AAS18443 represent contig DNA sequences that encode for
                                                                                                                                                                 Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0
                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding narbonolide polyketide synthases from Streptomyces narbonensis, useful for the recombinant production of polyketides, e.g. \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002
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                                                                                                                                                                                           S. narbonensis PKS
                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1998;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces narbonensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betlach MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Narbonolide polyketide synthase; PKS; narbomycin modification enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOSA-) KOSAN
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484
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CATCGTCGAGTCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
                                                                       CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGGCGGAGCTGGTCATCTCGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTGCTGCGCGCGCCGCCGCCAGCCCCAGGTGCTCGATGAGCAGCGGCGGCC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATGACCAGCTCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCGGAGGCGACTGCGGCGACCGCACCCCAGCCGCAGCCCACGCAGAGGCGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding
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                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rapamycin; tylosin; picromycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0107093P.
99US-00320878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00434288
                                                                                                                                                                                            enzymes
                                                                                                                      22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. narbonensis polyketide synthase
                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>;</u>
                                                                                                                        Score 34.8;
Pred. No. 22;
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                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                      BB
                                                                                                         52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methylmycin; neomethymycin;
                                                                                                                                                                 U; 0 Other;
                                                                                                                                   Length 1681;
                                                                                                            Indels
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RESULT 43
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AAS18438/c
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Best Local (
                                                                                                                                                                                                                                                Matches
  Streptomyces narbonolide polyketide
                             20-MAY-2004
                                                                            ADL91894 standard; DNA; 1681
                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to recombinant DNA vectors (cosmids) that encode for the narbonolide polyketide synthase (PKS) enzyme and various narbomycin modification enzymes from Streptomyces narbonensis. The recombinant DNA vectors can be used to produce recombinant ketide synthases and a variety of different polyketides (e.g. erythromycin,
                                                       ADL91894;
                                                                                                                                                                                                                                                                                           Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              rapamycin, tylosin, narbomycin, picromycin, methylmycin and neomethymycin) for use in agriculture, medicine and health. recombinant vectors may be used to produce polyketides in reyields. AAS18432-AAS18443 represent contig DNA sequences that
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Col 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding narbonolide polyketide synthases from Streptomyces narbonensis, useful for the recombinant production of polyketides, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Narbonolide polyketide synthase; PKS; narbomycin modification enzyme; erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethymy agriculture; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-065495/09.
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27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001
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                                                                                                                                                                                                                                                                                                                        narbonensis
                                                                                                                                              481
                                                                                                                                                                                              541
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                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                              66; Conserv
                                                                                                                                                                                      МĊ,
                                                                                                                                                                                                              CGAGATGACCAGCTCCGGCCGACTCGACCGATGAGCGAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding S. narbonensis polyketide synthase.
                                                                                                                                                                                                                                              Conservative
                          (first entry)
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                                                                                                                                                                                                                                                                                                                       PKS enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rapamycin; tylosin; picromycin; methylmycin; neomethymycin;
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99US-00320878.
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                                                                                                                                                                                                                                                      22.6%;
                                                                            BP
                                                                                                                                                                                                                                                        Score 34.8;
Pred. No. 22;
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 synthase
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                                                                                                                                                                                                                                                                                                                                polyketides in relatively high DNA sequences that encode for
coding
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                                                                                                                                                                                                                                         Indels
sequence
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RESULT 44
ADL91894/c
ID ADL918
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XX 20-MAY
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Best Local (
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     15-OCT-2002; 2002US-00271889
                                                                                                                                                                                                      narbonolide polyketide synthase medical application; industrial
                                                                                                                                                                                                                                                                       Streptomyces narbonolide polyketide synthase coding sequence #7.
                                                        16-OCT-2003
                                                                                                                                                   Streptomyces narbonensis.
                                                                                                      US2003194784-A1
                                                                                                                                                                                                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL91894 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.
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18-MAY-2001;
18-MAY-2001;
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(LIUH/)
(XUEY/)
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LIU H.
XUE Y.
ZHAO L.
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2001US-00860846.
2001US-00861289.
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55.9%;
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                                                                                                                                                                                              synthase gene; polyhydroxyalkanoate monomer; ndustrial application; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1681
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RESULT 45
AAS59803
ID AAS59
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Best Local :
                                                                                                                                21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EIISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence represent a Streptomyces narbonensis narbonolide polyketide synthase coding sequence of the invention.
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18-MAY-2001;
18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.
  Skeiky YAW, Per:
L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes immunogenic protein encoding DNA
                                                                                                                                                                                                                                                                                        01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium
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                                                                                  (CORI-) CORIXA
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XUE Y.
ZHAO L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAG 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                2000US-0199047P.
2000US-0208841P.
2000US-0216747P.
  Persing DH, |
e J, Zhang Y,
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2001US-00860846.
2001US-00861289.
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55.9%;
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Mitcham JL, Wang SS,
, Jen S, Carter D;
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                  particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAUG740-AAUG7444 and AAUG8011. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved infections of bone, joints and the central nervous system, however it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic polypeptides. The proteins and associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders
                                                                                                                                                                                                                                                                        Sequence 1498 BP; 286 A; 458 C; 450 G; 301 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS59506-AAS59804 represent DNA molecules encoding Propionibacterium acnes immunogenic polypeptides. The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 298; 1069pp; English
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                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
756
                                          90
                                                                                                                                                                                  64;
                                                                                                                                                                                                        Similarity
                                          CGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGAC 142
                                                                                        CCACTCGCGAGCTGGCGCCGATCCCGTCCCTGCTCCTCACCTAGCTATCCACCACCACC 755
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                                                                                                                                                                                                 22.5%;
56.6%;
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                                                                                                                                                                                                      Score 34.6;
Pred. No. 25
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                          25;
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Result
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Maximum
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Perfect score:
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1: gb ba:*

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154
1 cggccggagctaatce
    Query
Match
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                                                                                                                   Stecca, K.L.
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Sequence 25
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154 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
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Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
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Nucleotide sequences of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other sequences; artificial sequences.
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ilarity 100.0%;
Conservative (
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Pred. No. 1.1e-19;
D; Mismatches 0;
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Pred. No. 1.1e-19;
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AX353724
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ACCESSION
                                         RESULT 6
AX353724/c
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AX353724
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Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
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AX353724
                                                                                                                                                                                                                                                                                                                                                                                  Allen, S.M., Butler, K.H., Carlson, T.J. Plastidial phosphoglucomutase genes
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nt: EP 1174510-A 17 23-JAN-2002;
du Pont de Nemours and Company
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region
                                                                                                                                                                                                                                                                                organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Pred. No. 1.1e-19;
; Mismatches 0;
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EP1174510.
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EP1174510
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delta-9
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ACCESSION
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AX392337/c
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AUTHORS
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Best Local Similarity
Matches 84; Conser
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Matches 11
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112; Conserv
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AX392337
Sequence 26 from Patent
AX392337
AX392337.1 GI:19700690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified unclassified.
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Sequence 26 from Patent
AX392337
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Patent: EP 1174510-A 17 23-JAN-2002;
E.I. du Pont de Nemours and Company
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Patent: WO 0216565-A 26 28-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. Nucleotide sequences of a new class of diverged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen, S.M., Butler, K.H., Carlson, T.J. and Plastidial phosphoglucomutase genes
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                                                                                                                                                                         CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
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                                                                                                                 CATCGTCGAGTCGGCGGCCGCTGAGT 5433
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   /mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Plasmid pBS68"
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/mol type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                             organism="unidentified"
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/db_xref="taxon:32630"
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97.7%;
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Pred. No. 1.6e-06;
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AX367144
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Recombinant constructs and their use in reducing gene expression

Patent: WO 0200904-A 29 03-JAN-2002;

E. I. du Pont de Nemours and Company (US) , PIONEER HI-BRED

INTERNATIONAL, INC. (US)
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AX367144
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Patent: WO 0216565-A 26 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
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                                                                                                   CGAGATGACCAGCTCCGGCCG 154
                                                                                                                          GCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAG
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 29
                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol_type="unassigned DNA"
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/db_xref="taxon:32644"
/note="Plasmid pBS68"
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Pred. No. 1.6e-06;
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963 bp
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5.1e-06;
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                                                                                                                                                                                                                                                                                           and Nichols, S.E.
Recombinant constructs and their use in Patent: WO 0200904-A 12 03-JAN-2002;
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E. I. du Pont de Nemours and Comman: ''''' ------
                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                         other sequences; artificial sequences.
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GAGATGACCAGCTCCGGCCG
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                                                                                                                                                                       /note="ELVISLIVES complementary region of pKS106 and pKS124"
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/db_xref="taxon:32630"
/noTe="ELVISLIVES complementary region of pXS149"
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Sequence 12 from Patent WO0200904.
AX367127
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Patent: WO 0216565-A 24 28-FEB-2002;
E. I. du Pont de Nemours and Company
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Sequence 24 from Patent WO0216565.
AX392335
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Recombinant constructs and their use in reducing gene expression Patent: WO 0200904-A 12 03-JAN-2002;
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 GAGATGACCAGCTCCGGCCG 117
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/mol_type="unassigned_DNA"
/db_xref="taxon:32630"
/noTe="ELVISLIVES complementary
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/mol_type="unassigned DNA"
/db xrefs"ttaxon:32610"
/note="ELVISLIVES complementary region
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Sequence 14 :
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and Nichols, S.E.
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other sequences; artificial sequences.
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Patent: WO 0216565-A 24 28-FEB-2002;
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larity 100.0%; I
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                                                                                                      /organism="synthetic construct"
/mal_type="unassigned DNA"
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/note="ELVISLIVES PCR primer"
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/mal_type="unassigned DNA"
/db xrefe"ttaxon:32630"
/note="ELVISLIVES complementary
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RESULT 17
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Sequence 24 from Patent WO0200904.
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AX367129
 . Similarity 47; Conserv
                                                                                                                                     Recombinant constructs and their use in reducing gene expression Patent: WO 0200904-A 24 03-JAN-2002; E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                              note="ELVISLIVES complementary
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                                                                                                                                                                                                  Gordon-Kamm, W.J., Kinney, A.J.,
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 Score 45.8; D
Pred. No. 21;
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Matches 47; Conserv
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Direct Submission
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Glassman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Low and Nichols, S.E.
Recombinant constructs and their use in reducing Patent: WO 0200904-A 24 03-JAN-2002;
E. I. du Pont de Nemours and Company (US); PIONE INTERNATIONAL, INC. (US)
Location/Qualifiers
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                                     Kharel, M.K., Lee, H.C., Liou, K., Woo, J.S. and Sohng, J.K. An approach for cloning biosynthetic genes of 2-deoxystreptamine containing aminocyclitol antibiotics: isolation of biosynthetic gene cluster of tobramycin from S. tenebrarius
                                                                                                                                                                                                                                                                                               Streptomyces tenebrarius
Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                            2-deoxy-scyllo-inosose aminotransferase; 2-deoxy-scyllo-inosose synthase; carbamoyltransferase; dehydrogenase; glycosyltransfera ORF1; ORF2; ORF3; tacA gene; tacD gene; tbmA gene; tbmB gene; tbgene; tbmD gene; tbmB gene; transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces tenebrarius strain ATCC 17920.
                                                                                                                                                                     cluster from Streptomyces tenebrarius FEMS Microbiol. Lett. 230 (2), 185-190
                                                                                                                                                                                                                                                    Kharel, M.K., Basnet, D.B., Lee, H.C., Liou, K., Woo, J.S.,
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(bases 1 to 13802)
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/mol_type="unassigned DNA"
/mol_traxon:32630"
/note="ELVISLIVES complementary
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/tranelation="MPPHLAINGTPVRTRPWPVWPQPARGALDALERVLRSGRWAIS
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                                                                                                                                                                                                     /product="putative aminotransferase"
                                                                                                                                                                                                                                                                                                                                                                           /gene="tbmB"
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RASGYTHQDHAVVEAVLDGTPLPHSAVEAWTSARVLEAAAESAATGRTVELAPSPNGH
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GLVLAHGSNEVHSPKERRVRELVADADAFGRPHLARVVVRNGGPDSGWCLDPALAGGG
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IAAEKGVEFFVEAAAELRRRGRRCRFLVAGDGFTRQEIEKLAEDRGVADRITITGFLP
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PPFDTPAMADAIEALLDDPELRERIAETAAPLPSAKYSLTTAADQLTDIYRELGVCV"
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YGWLIARALGVPLVAQIHSSRPLSQHPTTLWERVTDPAAKWAERFTVRNAAAVLMLTE
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VPGAMSLGF FYEHVSEYTGLGGDN PGKLMGLAAHGTTVDETLSAFAFDSDGYRLAYLD
PQAEDPENMEDE SYTERAMFAHLER I YRLPPMEFVRRYD PAKGRVVRDTRAD FYEYLD
LAATAQAALERAVFGLADSVLARTGERTLFVAGGVGLNATMGKLLTRSTVDKMFVPP
VASD LGVSLGAAAAVAVELGDR I APMODTAMGFES PDQVRAALDRYGGLAYREPANL
ERE VJALI ASGKVVGMAQRGE VFFRALGORSLLGSAHSFTYRDHI NILRYKDREWMRP
FAPSMLRSVSDQVLEVDADF PYMIMTTKVRAAYAERLPS VPHEDWSTR PQTVTEASNP
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/gene="tacA"
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TAEIGFPISPAYAPLHTNRLYAPASRRRFALGEEHEKRIDPARFHLPVCERLTRRLIT
FHHAALLGDESDMHDIAAAVAKVLRHIGELRA"
GTLRSGRDPRTSVTDPFGRLHGYDNVWAVDGATFPFAGNPNPTLTIQANAHRIASAID
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APVQAAAFCLAQAGLTVDDLDAVAFGWDLPAMYRERLGGWPHSDSEALDILLPRDVFP
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complement (8582...9769)

/note="ORF2"
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RGSGARVHDWDGNAYLDLTCSFGTVLICHAEREVTDAIRACLDEGNLFYTGPSPRRLA
LAERLLDWFPWADQALFYRTGSCAVSSVARLSQHVTGRTAVLTSGYHGWHDWHLEAVP
EAKLFPSYATEFHDDLDVYRAYLDRHADBIAAVVTPEPFRHPLEHYRTLRDLAAEAG
CLFVLDEVKTGMRAGKGGLSAAAGLEPDAVTVSKGLANGHSISAVVGSRRITEGLAEAE
HVWSTYQNEGVGYAAALSTVDFLLREDVAGVVERTGRTVBBAFRSAFAERGLEVEVHG
WGPWPDLDFSAAEEDLPERLQLALLRHGVFCDVGDDFNLMYRMADHLDELLERVTAAI
ASV"
/gene="tbmE"

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JOURNAL
REFERENCE
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AUTHORS
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Best Local (
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Streptomyces tenebrarius
Streptomyces tenebrarius
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Submitted (01-AUG-2003) Sohng J.K.,
                                                                                                                                          Kharel, M.K., Lee, H.C., Liou, K., Woo, J.S. and Sohng, J.K. An approach for cloning biosynthetic genes of 2-deoxystreptamine containing aminocyclitol antibiotics: isolation of biosynthetic gene cluster of tobramycin from S. tenebrarius
                                                                                                                                                                                                                                                                                                               Isolation and characterization of the tobramycin biosynthetic gene cluster from Streptomyces tenebrarius FEMS Microbiol. Lett. 230 (2), 185-190 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2-deoxy-scyllo-inosose aminotransferase; 2-deoxy-scyllo-inosose synthase; carbamoyltransferase; dehydrogenase; glycosyltransferase; ORF1; ORF2; tacA gene; tacD gene; tbmA gene; tbmB gene; tbmC gene; tbmC gene; tbmD gene; tbmB gene; tbmC gene; tbmD gene; tbmB gene;
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                                                             sohng, J
                                                                                                                Unpublished
                                                                                                                                                                                                                                Kharel, M.K.,
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                                Submission
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ERVAVLGAGGIGLMLMQVARQRGGVITTVGEPVAERRAVAAQLGARTVTTGRFCELAE
LVAKHPDLTPDVVLEASGYPVAVGBALEVVRPGGRIGLVGYRVEEVGPWATHHVAVKA
LTIRGSLGPGGRFPEAIDLLARGEIEVEPLLSHEFALDDHARALDLALRRAEGNVRSF
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RGVWHGFSYPVVPGHEWSGTVVEVNGPGAELVGRDVVGDLTCACGSCAACGRGTPVLC
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transl_table=
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(product="putative dehydrogenase")
(protein id="CAB22477.1"
(db_xref="GI:45544457")
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58.8%;
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                      Lee, H.C., Liou, K., Woo, J.S., Kim, B.G.
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Chemistry,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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Sun Moon University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene cluster,
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                    /translation="MPVHLAINNGTPVRTRPWPVWPQPARGALDALERVLRSGRWAIS
GPYRGIESAERRFARDFAAYNGVAHCVPAASGTASLMLALESCGVGVGDEVIAPGLSW
VASASTIVGVNAVPVLVDIDPRTLCLDPAAVEAAITPATKAVVVVVHLYSAVADLDALR
                                                                                                                                                               aminotransterase"
                                                                                                                                                                                                                                                                                                      complement (3684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="tbmA"
                                                                                                       /protein_id="CAE22472.1"
/db_xref="GI:45544452"
                                                                                                                                                                                      product="putative
                                                                                                                                                                                                                                                                                                                                                                 complement (3684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVPDAVRGGDRVH"
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/product="putative deh
/protein_id="CAE22470.
/db_xref="GI:45544450"
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transl_table=
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db_xref="taxon:1933"
country="Mexico"
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strain="ATCC 17920"
                                                                                                                                                                                                                       _table=11
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                                                                                                                                                                                                                                                                                                         .4958)
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                                                                                                                                                                                                                                                                                                                                                                 .4958)
                                                                                                                                                                                      2-deoxy-scyllo-inosose
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VEVLADITAMLGTLPVREIRSGLCEVVKNALAIRPSMIDFLÄAELRĖDGRYADDVLRWM
IDESVAAKAQVTEHKXTERRECIVASYHTVOHALEHASHGAVSHGAGYGVGMVAAAE
VARRLGHVDADLVELHRELYGKVGVATTLPADVFTEEITYRLGFDNKRGYQPLFADHY
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GGGVTGNIAGLLAALLFRGIRLVHVPTTVVAMLDSVLSLKQAVNAQVGKNLVGTFYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGGVHAEVFAEHPRARLAAVCDLDRGAARELAGRFAVETVTDDLDSVLSDRIGINVTTPNALHABQAARALRAGRHVLVEKPLALTSDEIRGLLRLADERGLVLAHGSNEVHSPKFREVBELVADAAFGREHLARVVFNROGEDSGWCLDPALAGGEVLAHGSNEVHSPKFREVBELVADAAFGREHLARVVFNROGEDSGWCLDPALAGGEVLAULDLGCHAVEICRHLLGGAEVRAVTARSORVRPRAGRVEDQATLLLEFADGALGQCD
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                                                                                                                                                                                                                                                                                                                                    /product="2-deoxy-scyllo-inosose
/protein_id="CAE22471.1"
/db_xref="GI:45544451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RASGYTHQDHAVVEAVLDGTPLPHSAVEAWTSARVLEAAAESAATGRTVELAPSPNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSWACPGGEEITTEVLGTSGRAGADLWAGMGVHAFSERGFASVWEPNQGWVRPEWEWV
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HELIPSVMALSQLVVLPSRYEELGIVILECMSMRRPIVAHDVNGVHKLIEHGRTGLLV
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protein_id="CAE22469.1"
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470.1"
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/transl tak
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GGPI PRGADVEDHEDDDGWAFARRHGRETROGFPWTAWALGGGTVFYAGMSYRYODSD
LAPPSSLLGEADYDHWQVGLADLEPHYEWIE ZYQLAVAGPSRKRYGDYVF PVYHRPSLF
PTPPGLALAEGARALMI.TPLPTPVA.16GIRDRFGPGCAQATFCTSFSCCTGAKADVVS
RVLAPAEGDVSVLVHTRVDRLVASGSHRVDAAEVVDRGTGTRRTLRARRFLVAANA.1Q
SAALLLESTSRLEPDGLGNGNGLVGRHLAMKNSVYVRGVVPRRLLFGYTPLRHRYSSVC
VLDYLTGEEFPDGVGGLIHEANPWEPJALEREAERGTVLAVERLLGDRPQARNRVRLSR
TRDRDGFPRIVLDYEPHPADLTRLAVLSERATDILTKAGAIDVREVDTAYELGSAHLH
GTLRSGRDPRTSVTDPFGRLHGYDNVMAVDGATFPFAGNPNPTLTIQANAHRIASA.1D
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                                                     /transl_table=11
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/product="putative transport protein"
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/transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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EAKLFPSYATEFHDDLDVYRAYLDRHADEIAAVVVTFEFTRHFLEHYRTLRDLAAEAG
CLFVLDEVKTGMRAGKGGLSARAGLEPDAVTVSKGLANGHSISAVVGSRRITEGLAEA
CLFVLDEVKTGMRAGKGGLSARAGLEPDAVTVSKGLANGHSISAVVGSRRITEGLAEA
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RRTDPPLHFVQHHLAHAASAYYFSGEDRGAVLLVDGQGEEECYTLAHABGGKITVLDT
VPGAWSLGFFYEHVSEYTGLGGDNPGKLMGLAAHGGTTVDETLSAFAFDSDGYRLLNIL
DQARDEDWDDEYSVTERAWFAHLERIYKLPPNEFVRKYDPAKGRVVRDTRRDPYSYRD
LAATAQAALERAVFGLADSVLARTGERTLFVAGGVGLNATMNGKLLTRSTVDKMFVPF
VASDIGYSLGAAAAVAVELGDRIAPMGTAAMGEPES PDQVRAALDRTGLAYREPANL
EREVJALIASGKVVGWAQGREEVFRALAGRSLLGSAHSPTWRDHINLRVKDREWMF
ERAPSMLRSVSDGVLEVDADFPYMIMTTKVRAAYAERLBSVVHEDWSTRPQTVTEASNP
FAYHRWLTELGDLVGDPVCLNTSFNDRGEPIVSSPADALLTFSRLPIDALAVGPPYLVTK
   AVGVSFGLVQMALVLADTRLQDAITGPARATVTSVVGFGSEVASVGFYLAAGAVSTVT
SMSTLVAMFAVPLVLIAVVAFRWLRREPCPTGQVRPEPBPRRRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (9909.
/gene="tbmE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVWSTYQNEQVGYAAALSTVDFLLREDVAGVVERTGRTVERAFRSAFAERGLPVEVHG
WGPMFDLDFSAAEEDLPERLQLALLRHGVFCDVGDDFNLMYRMADHLDELLERVTAAI
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NALRRANAELLNTLLAEQGLRQATS FGTTSRTYYVYAABLPDDAFVGLPITTVTEAL
TAELGFP18PAYAPLHTMRLYAPASRRRFALGEEHEKRIDPARFHLPVCERLTRRLIT
FHHAALLGDESDMHDIAAAVAKVLRHHGELRA"
                                                                                                                                                                                                                                                                                                                                                                                                                           complement (9909.
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                                                                                                                                                                                                                                                                                                                                                            /gene="tbmE"
/codon_start=1
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="tacA"
/codon_start
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="ORF2"
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Best Local S
Matches 90
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                                                     BX571966 10
BX571966 11
BX571966 13
BX571966 13
BX571966 14
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BX571966 19
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BX571966 00
BX571966 01
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BX571966 04
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/product="putative dehydrogenase"
/protein_id="CAE22477.1"
/db_xref="GI:45544457".1"
/db_xref="GI:45544457"
/translation="WKALSFEAPGEAVFGTREVPVPAPGEALIHLGYNSICGSDLSLY
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ERUMELGFTRDGACAEYMTIFTGGNLHVLPEGLSLRAACQVEFVAVALHAVSTYGVEPG
ERUMPLGFTRDGACAEYMTIFTGGNLHVLPEGLSLRAACQVEFVAVALHAVSTYGRPGELAE
ERVAVLGAGGIGLMLMQVARQRGGVITTVGGFVAERAVAQLGARTVTTGRFDELAE
ERVAVLGAGGIGLMLMQVARQRGSAIEVVRPGGRIGLVGXXVEEVGFWATHFVAVKA
LTIRGSLGPGGRFFEAIDLLARGEIEVEFLLSHEFALDDHARALDLALRAEGNVRSF
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/gene="tacD"
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/transl_table=11
/product=-hypothetical_protein"
/protein_id="CAE22478.1"
/db_xref="GI:45544458"
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Best Local :
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BX571966 02
BX571966 03
BX571966 04
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Pred. No. 2.2e+02;
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Pred. No. 2.2e+02;
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AUTHORS
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SOURCE
ORGANISM
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VERSION
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AE004846
LOCUS
                                                                                                                                            FEATURES
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JOURNAL
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MEDLINE
PUBMED
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                                gene
 Sg
                                                                                                                             source
                                                                                                                                                                                                                        accuracy of the protein name.

Class 1: Function experimentally demonstrated in P. aeruginosa.

Class 2: Function of highly similar gene experimentally
demonstrated in another organism (and gene context consistent
in terms of pathways its involved in, if known).

Class 3: Function proposed based on presence of conserved amino
acid motif, structural feature or limited sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 10348)
Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,
Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J.,
Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E.,
Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N.,
Folger,K.R., Kas,A., Larbig,K., Lin,R.M., Smith,K.A., Spencer,D.,
Wong,G.K.-S., Wh,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
Hancock,R.E.W., Lory,S. and Olson,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E. Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z. and Paulsen, I.T.
                                                                                                                                                                                                                                                                                                                                                                                             Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics,
University of Washington Genome Center, University Of Washington,
Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of Pseudomonas aeruginosa PA01, opportunistic pathogen Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa Community Annotation Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa PAO1
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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AE004846.1 GI:9950517
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                                                                                                                                                                            Homologs of previously reported genes of unknown function, no similarity to any previously reported sequences.
                                                                                                                                                                                                                  an experimentally studied gene.
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section 407 of 529 of the complete
                                                                                                      aeruginosa PAO1'
                                                                                                                                                                          sequences.
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name confidence: Class 4 (homologs of
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Local Similarity
8072 AGCGGCTGGÁCCÁGGTGCGGGGTGÁCGÁTCATCAGCAGC 8110
                                                                                                                      8012 CCCGGATCGTAGTGCCGCAGGCCCTCGCCGGCAGGTCCGGCAACTGTGCGTCGGCGGCC 8071
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complement (5483. .6748)

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LQVDFLNDCCGYLRQMLRQGGSARSTLLTIKQLFEDRRLTTIQERIGKLSAKMSLVMM
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Pred. No. 4.2e+02;
0; Mismatches 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stover.C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  accuracy Class 1: Class 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.
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AE004846.1 GI:9950517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 186, Canada
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1 (bases 1 to 10348)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-FEB-2003) Department of Molecular Biology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa Community Annotation Project (PseudoCAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein name confidence' is used to rate our confidence of the accuracy of the protein name.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 10348)
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(bases 1 to 10348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: Function experimentally demonstrated in P. aeruginosa.
2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).
3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                 to an experimentally studied gene.
4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
   based on
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
/locus tag="PA4296"
/note="Protein name confidence: Class 3 (function proposed
based on presence of conserved amino acid motif,
                                                                                                                                                                                                                                                    Tom/
                                                                                                                                                                                                                                                                       organism="Pseudomonas aeruginosa PAO1"
                                                                                                                                                                             db_xref="taxon:208964"
                                                                                                                                                                                                                mol_type="genomic DNA"
strain="PAO1"
                                                                                                                          Locus
                                                                                          us_tag="PA4296"
.919
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structural feature or limited sequence similarity to experimentally studied gene)"
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/transI_table=11
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NATISAGTGLASVNSGQSALLNPILGGLLGTHIDLSAAAYNGIADAKLSVLDIIGADG
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EPKRIVSGPPGQDESGAWRTEVRQSQVFLTADIDGGFLSILATTKLQLAIEGASGAVW
LKSMACTRPDTALDFGRSGATIKIGSPANIDQVGSILVLGGLVRLDLKLDTSIAGS
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SGDTRRNVKADGSDLVQSRRLPESGFLASTLKTSINVNFVVLGLCLPLLCGSTALTDL
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DIHKIIYEVHGNSQPEALRSEDSQPSAPPAPVAESQVSPSNPLFGKLSPRQQAVARLV 
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/locus_tag="PA4299"
complement (2947. . 3684)
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/notes_Teyrotein name confidence: Class 4 (homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences)"
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/locus tag="pA4298"

/note="Protein name confidence: Class 4 (homologs previously reported genes of unknown function, or similarity to any previously reported sequences)"
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complement (2640. .2924)
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complement(945..2615)
/locus_tag="PA4297"
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previously reported genes of unknown is similarity to any previously reported
                                                                                                                                    complement (3681..4592)
/locus_tag="PA4300"
complement (3681..4592)
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                                                                                                                                                                                                                                      AAPASDDPLAELPAEANMHTAMANEAP"
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                        AP005046 301925 bp DNA linear ECT 10-MAY Streptomyces avermitilis genomic DNA, complete genome, section 26/30.
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AP005046 BA000030
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                                                                                                                                                                                                    GGACCTGCCCGGCGAGGGCCTGCGGCACTACGATCCGGG 8012
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSTGFGARPDGGAFHSRQEQDIQALKLRLHRYIIDEIDEDGMNL
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MEMLVGLTGNRLPEQTLRLMICAALDVVVQITRLASGRRCISEVLEVLEVRDGVYVTN
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vavrprsshmilarqmrragicrorerpelicalilivescusligitilalgelilar
LSCRVALGMLYQRRLKRMIRQMPRFLDQVVRSLHAGRTIGALMQAVENAEEPLRDIF
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EREKLJSRQLHAMTGETRISAYVLAGVPSALGGYILASNPGYLLNMWADGTGRFLLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLFSLDRRGSGQFVRQAAPVGQKFRQALL"
complement (6745. .7929)
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complement(4602..5
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LQVDPLNDCCGVLRQMLRQGGSARSTLLTLKQLFEDRRLTTLQERIGKLSAKMSLVMM
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LFVLLVLLVKLLRAESEASYAVPLLFAAGIGFLLPKQVLKHFAKARRALIADEMILFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (6745.
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Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayum Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T., Kushida, N., Director-General of Biotechnology Center, Shiba, T., Sakaki, Y. and Hattori, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Following url is also available. http://avermitilis.ls.kitasato-u.ac.jp.
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Submitted (29-MAR-2002) Director-General of Biotechnology Center,
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Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
mat. Biotechnol. 21 (5), 526-531 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and J. Ishikawa.
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*5 School of Science, Kitasato University
*6 Institute of Medical Science, University of Toky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *1 Kitasato Institute for Life Sciences, Kitasato University
*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
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65; Conserv
  Streptomyces avermitilis MA-4680
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AP005046 301925 bp DN Streptomyces avermitilis genomic DNA,
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AP005046.1 GI:29609904
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note="CYP107X1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="cyp23"
7611. .8777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=11
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59.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38;
Pred. No. 2
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                                                                                                    DNA
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                                                                                                    linear
                                                                          genome,
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-MAR-2002) Director-General of Biotechnology Center, Mational Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
This work was done in collaboration with Haruo Ikeda (*1), Jun Ishikawa (*2), Akiharu Hanamoto (*3), Chigusa Takahashi (*3), Mayumi Shinose (*3), Hiroshi Horikawa (*4), Hidekazu Nakazawa (*4), Tomomi Osonoe (*4), Norihiro Kushida (*4), Hisashi Kikuchi (*4), Tadayoshi Shiba (*5), Yoshiyuki Sakaki (*6,*7), Masahira Hattori (*1,*7) and Satoshi Omura (*1,*3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Kikuchi,H., Shiba,T., Sakaki,Y., Hattori,M. and Omura,S. Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Following url is also available. http://avermitilis.ls.kitasato-u.ac.jp.
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*1 Kitasato Institute for Life Sciences, Kitasato University

*2 National Institute of Infectious Diseases

*3 The Kitasato Institute

*4 National Institute of Technology and Evaluation

*5 School of Science, Kitasato University

*6 Institute of Medical Science, University of Tokyo

*7 RIKEN, Genomic Sciences Center
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Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
Kushida,N., Director-General of Biotechnology Center, Shiba,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M. Genome sequence of an industrial microorganism Streptomyces averantilis: deducing the ability of producing secondary
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Omura, S., Ikeda, H., Is
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     Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
                                                                                                                                                                                                                                                                                                                                              /note="This strain is also named as strain: ATCC 31267,
NCIMB 12804 or NRRL 8165.~synonym: Streptomyces
avermectinius"
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complement (828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Streptomyces avermitilis MA-4680"

mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain="MA-4680"
                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:227882"
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VLALVMVGGEPQASWNRI GETALACA LVLLVGHLPTPQQRGGGVRARLARAHDAAHAY
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aeqlravgsdlahvvstdvyvvsgepavlsavwdvveasglsigphsstligvaclgy
LVDTTTACAVHLDDAGRLPARHRERIAELLAELTDAHEHAGLDTPEAPRLPVAV"
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                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative integral membrane protein"
/protein_id="BAC73959.1"
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Arragrrpyptrydrsfaayyfpralgahfwspyesaaradlrtprtaackllraapp
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/protein_id="BAC73956.1"
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transl_table=11
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="SAV6246"
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Dalal, V.,

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KEYWORDS
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                                                                                                                                                                                                                                                                                                   DEFINITION
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                                                                                       ORGANISM
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Best Local
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                    AC134925 148829 bp DNA Oryza sativa (japonica cultivar-group) OSJNBa0041J17, complete sequence.
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VRIAVRDEGCAPGEPHESPQREEEHGRGLLLIASLCRAWGALETGPGLLVWADLERR
AAPPAPRDLSRSGDRSRSTTAASYCLAADSDDASRSPAENTEARSDLGWSAKKTPAES
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/note="SAV6251"
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/trans1_table=11
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/protein_id="BAC73963.1"
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/db_xref="GI:29609913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative cytochrome P450"
/protein_id="BAC73960.1"
/db_xref="GI:29609912"
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Pred. No. 2.4e+02;
0; Mismatches 45
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This sequence was finished as follows unless otherwise noted: all regions were either double-estranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi and was completed to phase III by the Cold Spring Harbor Laboratory Genome Center under the Indo-US collaboration. Clone OSJNBa0041J17 overlaps clone OSJNBa0007D07 from base 10381 to base 148829. The overlap is from base 1 to base 48448 on OSJNBa007D07.
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Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K., Aghar, A.K., Dalal, V., Batra, K., *McCombie, W.R., *Spiegel, L., *de la Bastide, M., *Zutavern, T., *Muller, S., *Nascimento, L., *Balija, V., *Bell, M., *Zutavern, T., *Muller, S., *Andrade, M.V., *Dike, S., *C'Shaughnessy, A., *Palmer, L., Gaikwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.

Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone OSJNBA0041117, complete sequence
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1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
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/note="The assembly is covered by high generated from a transposed plasmid subsequences of the state of the s
                         derived from a PCR product.
34119. .34200
                                                                                                                                                                                                                                                                                                                             /clone="OSJNBa0041J17"
/clone_lib="HindIII"
5865.__5934
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"

/mol type="genomic DNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="11"
                                                                                                                                                                                                                                                                                        note="The assembly is covered"
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AC134925/c
LOCUS
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                                                                                                           AC134925 148829 bp DNA Oryza sativa (japonica cultivar-group) OSJNBA0041J17, complete sequence.
                                                             AC134925
AC134925.4 GI:45598398
     Oryza sativa (japonica cultivar-group)
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                                                                                                                                                                                                                                                                                                                    CTCCGACGCCGGGAGCGACGTGCAGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
                                                                                                                                                                                                                                                                                                                                                                        ACTCGACGATGAGCGAGATGACCAGCTCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCGCGCCGGCGGCCATCGCCCTGCCGTCCCTCGAGACGCTGCTCCTCGCCCCGCGT 68637
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/note="The assembly is covered by high quality sequences
/ note="Tom" a DCB product."
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derived from two transposed plasmid subclones."
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Pred. No. 4.3e+02;
0; Mismatches 70
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3 (bases 1 to 148829)
3 (bases 1 to 148829)
Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K., Ghazi,I.A., Yadav,M., Sureshbabu,K., Srivastava,S., Pal,A.K., Dalal,V. Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
Direct Submission
Submitted (28-FBB-2003) IIRGS, NRC on Plant Biotechnology, Indian Apricultural Research Institute, LBS Centre, New Delhi, Delhi
                                                                                                                                                                                                                                                                                                                                                                                                                                           regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, Such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi and was completed to phase II by the Cold Spring Harbor Laboratory Genome Center under the Indo-US collaboration. Clone OSJNBa001J17 overlaps clone OSJNBa0007D07 from base 100381 to base 148829. The overlaps from base 1 to base 48448 on OSJNBa0007D07.
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Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone OSJNBa0041J17, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (bases 1 to 148829)
Ghazi, I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K.,
Ghazi,I.A., Dalal,V., Batra,K., McCombie,W.R., Spiegel,L., de la
Bastide,M., Zutavern,T., Muller,S., Nascimento,L., Balija,V.,
Bell,M., Miller,B., Katzenberger,F., Andrade,M.V., Dike,S.,
O'Shaugnessy,A., Palmer,L., Gaikwad,K., Sharma,T.R., Mohapatra
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-MAR-2004) IIRGS, NRC on Plant Biotechnology, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agricultural Research Institute, LBS Centre, New Delhi, Delhi
110012, India
On Mar 21, 2004 this sequence version replaced gi:28604232.
This sequence was finished as follows unless otherwise noted: all
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Submitted (02-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi
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Ghazi, I.A., Yadav, M., Dixit, R.,
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1 Bungtown Road, Cold Spring Harbor,
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/note="The assembly is covered by high quality sequences generated from a transposed plasmid subclone." 66330. .66375
                                                                                                                                                                        /clone="OSJNBa0041J17"
/clone_lib="HindIII"
5865. .5934
                                                                                                                 derived from a PCR product
                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
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Dalal, V.,
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/note="The assembly is covered by
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                       CGCCTCGCGGGTGACCGGGTCGACGCTGGCCGGCATGTCCACCCGTCGCGGC
                                                                                     GGGCTCGGGCACCTTCTCGTCGCCGAACCAGAAGCCGGCGCTGATCACCTCCCGCGAGTA 18323
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Larimer, F.W., Chain, P., Hauser, L., Lamerdin, J., Malfatti, S., Do Larimer, F.W., Chain, P.A., Beatty, J.T., Lang, A.S., Tabita, F.R., Gibson, J.L., Hanson, T.E., Bobst, C., Torres, J.L., Peres, C., Harrison, F.H., Gibson, J. and Harwood, C.S.
Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris
Nat. Biotechnol. 22 (1), 55-61 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       genome consortium, the DOE Joint Genome Institute, Production Genomics Facility, Sel00 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laborato 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas
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Rhodopseudomonas palustris CGA009
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
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Larimer, F.W. and Harwood, C.S.
Rhodopseudomonas genome consortium
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                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
codon_start=1
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79. .2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2200001
2300001
2400001
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2000001
2100001
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1300001
1400001
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of AE016822 from
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Pred. No. 5.4e+02;
D; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2010000
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genome;
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EIGIELSTGKIRFTLGNVLTSKLLDGTFDYGRVIPQNNDKELLVDKKDFBAAVDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVPTRFLKSWIQTHYSDKVLSCWQAELPEVNRVDLTVRSPVRCATPAKEVPAPVESRR
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DEQRESAERSWGATFVSANHDALGGSFLDPRLTFASFVVGRSWILAHAAAKQVAEGRR
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Citation: Proteomics from VerBerkmoes et al.
                                                                                                  "npublished
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AQIEGEVAVLKLADPGSPTLIQDRDSKSALYVLMPMRV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="recf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locus_tag="RPA0002"
332. .3450
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function="InterPro IPR001238:IPR001687:IPR003395 COGs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSNMEQDRWSRVKGRLRSSVGEDVYSSWFARMDLESVHDESVHI
                                                                                                                                                                                                                                                                                                                                      gene="gyrB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="recF"
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                                                                                                                                           from VerBerkmoes et al. (2003)
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TAVLSVKVPDPKFSSQTKDKLVSSEVRPVVENVINEALAAWLEEHPSEAKIVIGKVVE
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/transl_table=11

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with PAS/PAC domains"

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complement (9442. .10893)
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GDADYVLKAVLRDLKGLSELVNNVLMPHQSVAHVRSSIVLDRLKESARLPVKLLANG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / trainal at i on="Mobephida Opatis addinimgtidge betwerahddrachtijekim
gesluakhetikals vyrogduny lunid degthytid pytahefocap marervudakoay
berais elgaedakovtaao atluvpaikoi gosllyfud ygakosaydare dunoska
reagaglyyidhlytinvyhrormdywtopyaklener Qirfed i borasglesralitse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (7673. .8791)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKGVALQRYKGLGEMNPSQLWETTLDTNARSLLQVKVREVDEADDIFTKLMGDVVEPR
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function="InterPro IPR000485 COGs COG1522"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function="InterPro IPR000014:IPR001687
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Larimer, F.W., Chain, P., Hauser, L., Lamerdin, J., Malfatti, S. Land, M.L., Pelletier, D.A., Beatty, J.T., Lang, A.S., Tabita, F. Gibson, J.L., Hanson, T.E., Bobst, C., Torres, J.L., Peres, C., Harrison, F.H., Gibson, J. and Harwood, C.S.

Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris Nat. Biotechnol. 22 (1), 55-61 (2004)
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14704707
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                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas genome consortium, the DOE Joint Genome Institute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodopseudomonas palustris CGA009
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Larimer, F.W. and Harwood, C.S.
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/note="observed by proteomics
Citation: Proteomics from Ver
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/gene="kaiB"
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vslglvfhelttnavkygalsvpsgrisvrrvgatdealtiewoehdgppvtppossg
/transl_table=11 |
|product="chromosomal replication initiator protein DnaA"
                                                                                                                                                                                                                                                    organism="Rhodopseudomonas/mol_type="genomic DNA"/strain="CGA009"
                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                       evidence=not_experimental
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                                                                  codon start=1
                                                                                   locus tag="RPA0001"
function="InterPro IPR001957:IPR003593 COGs COG0593"
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79. .2097
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58.9%;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                              palustris CGA009"
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KATDLDLEVTETLPAETATAGSTTVPAHMYDIVRKLDDGSQTVLESDGDRSVLAIRA
GRSRFTLQTLPESDFPDLAAGEMSHAPRLPASDVKRLIDRTQFAISTEETRYLLNGI
LHTAGSPKASSLRAVATDGHRLAQLDLTLPSGADGMPGVIVPRKTVGEVQRLIEDTEA
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DEQRESAERSNGATPVSANHDALGGSPLDFRLTFASFVVGRSVTLAHAAAKQVAEGRR
GDPWENPLY IHSGVGLKTHLLQAVTWAGNAGTERKVLYLTAEKFMYGPVAALKTOF
SLAFKEALRGIDVLVIDDLQFLQGKTTQAEFCHTLNALIDAGRQVVVAADRPPADLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGKTNCLEAISFLSPGRGLRRATLEDVANHEGDGSWAVSTEIEGALGLATLGTGIEP
PRGDTTTTRCRIDREPVGSAAAFGDHLRMVWLTPSMDGLFMGAASERRRFFDRLVLA
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HNGRDLEGAINRLLAHSKLNNQPVTLEMAEHEVRDLIRPSEPKRIKIEDIQRIVARQY
NVSRSDLLSSRRTANVVRPRQVAMYLAKTLTLRSLPEIGRRFGGRDHTTVLHAVRKIE
                                                                                                                                                                                                                             Citation:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAAMLDARGATSAFPSAKLMLDGWMENALTSEPATAVEDRYRAILRDSRGRDAAAGRT
LDGPHLTDLEVIYAPKAMPARDASTGEQKALLIGLVLAHAQLVAETTSITPLLLLDEV
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/product="DNA polymerase III beta subunit"
/protein_id="CAB25446.1"
/db_xref="GI:39652707"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative RecF protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="InterPro IPR001001 COGs COG0592"
/note="observed by proteomics
Citation: Proteomics from VerBerkmoes et al.
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/function="InterPro
IPR000565:IPR001241:IPR002288:IPR003594:IPR006171 COGs
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/transl_table=11
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      /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .DSGHSARVSALDRSLRSRNRLLEDVRNADSHWLDAIERETAELAIAVAAQRGQTALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSFRARTSSMTAARITRLTLTHFRNYRGASLTTTADQVVLVGPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus_tag="RPA0003"
function="InterPro IPR001238:IPR001687:IPR003395 COGs
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                                                                                                                             evidence=not_experimental
                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                       note="observed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="gyrB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Locus_tag="RPA0004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSERGRAVKLALSAGKLVLSVTNPDSGSATEELEVEYASDPLDIGFNSRYLLDIA
                                                                                                                                                                                                                    served by proteomics
Proteomics from VerF
                                                                                                                                                                                                                             from VerBerkmoes et al.
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cns

gene

SdC

CDS

gene

cps

FTGRIQALAATHTLLSNASWQNLHIRDVLAAELAPFASLSSGRIVTDGLDIAVDAKTA VSLGLVFHELTTNAVKYGALSVPSGRISVRRVGATDEALTIEWQEHDGPPVTPPQSSG

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SdC

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EVAAIDDAMLGSADARKLDEYAAVLQEVYPRPGVLRKKEAETAIHGPISLFEAVTDAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (9442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="4-hydroxyphenylpyruvate dioxygenase"
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transl_table=11
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litation: Proteomics from VerBerkmoes et al. (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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function="InterPro IPR000485 COG8 COG1522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function="InterPro IPR000014:IPR001687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus tag="RPA0007"
function-"T-
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917. .9396
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishikk, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Lu, M., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kayawa, J., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Saco, K., Shibata, K., Shibagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
E 2 (bases 1 to 674)

Adachi J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, R., Hiramoto, K., Hiraoka, T., Hayashida, K., Hayashizaki, Y., Ikeda, R., Imamura, K., Ishibaki, J., Ishia, Y., Ishikawa, M., Itoh, M., Kagawa, I., Imotani, K., Ishibaki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kodayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Koya, S., Kurihara, K., Matsuyama, T., Miira, J., Miyazaki, A., Masuda, H., Matsubara, K., Matsuyama, T., Mira, J., Miyazaki, A., Mamiki, T., Narikawa, R., Niikura, J., Nagata, T., Nakamura, K., Namiki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 CGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAG
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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Oryza sativa (japonica cultivar-group)
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/note="observed by proteomics
Citation: Proteomics from VerBerkmoes et al. (2003)
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Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A linear PLN 24-JUL-2003 cDNA clone:001-120-E01, full
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             SOURCE
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                                                                                                                                                                                                                     RESULT 36
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                                                                                                                            AKU63727 674 bp mRNA linear PLN 24-JUL
Oryza sativa (japonica cultivar-group) cDNA clone:001-120-E01,
     AK063727.1 GI:32973745
FLI_CDNA; oligo-capping.
Oryza sativa (japonica cultivar-group)
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Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Azakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashiaki, Y.
235 GCTTCGGGTCGGACTCGCGGTTCGGCGGCGGCGCCGACGACGACCTCCGG
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                                                                                                                                                                                                                                                           clone="001-120-E01"
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/db_xref="taxon:39947"
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japonica rice.
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FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Fujimura,T., Kuroaski,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Sugiyama,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
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                                                                                                                                                                                                                                                                                                                                                       Medical Center Dr, Rockville,
4 (bases 1 to 133449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buell, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medical Center 3 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC107207
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                      Submitted (01-JAN-2004) The
                                                             Direct Submission
                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                    Buel1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 133449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="001-120-E01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:37514985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dr, Roc
133449)
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Pred. No. 1.5e+03;
0; Mismatches 46
                              Institute for
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                              Genomic
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

25 1 (bases 1 to 133449)

26 See 1 to 133449)

27 28 Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,

Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S.,

Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S.,

Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V.,

Vang, Q.O., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J.,

White, O., Salzberg, S.L. and Fraser, C.M.

Oryza sativa chromosome 3 BAC OSJNBb0106M04 genomic sequence

UL Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ccedaeciedicaicicecicaiceiceaecedecedecedeaecideicaicicecicai
Submitted (04-OCT-2003) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA 5 (bases 1 to 133449)
                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (28-SEP-2002) The Institute for Genomic Submitted (28-SEP-2002) The 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCG
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1e 3 BAC OSJNBb0106M04 genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This BAC overlaps with rice BAC OSJNBa0079B15 (AC099043) and OSJNBa0072F13 (AC133450).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
On Oct 4, 2003 this sequence version replaced gi:23343713.
Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC clone OSJNBb0106M04 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC
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                                                                                                                                                                                                                                                                              complement (4843. .4899)
/rpt_family="Oryza"
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4843. .4901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MASQSRLTISGAHAFFPYLSFPEYSLIHRNLPAVSSPLPPVDGE
ASRPPGHRLHCLRPRPLPSRIVPTEAMEGRSKRRHRLGKPPPDLQAGAVGGCADGRGN
KGPAPPTSTSRGRATSHSSAPPRSCWTLTASHPPPRSAAGFALTTPFRVGVGTNRTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OSJNBb0106M04.1"
337. .912
     complement (4846. .4899)
                                                                                                                                                      complement (4844..4899)
/rpt family="Oryza"
complement (4845..4899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4843.
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/product="hypothetical protein"
/protein_id="AAR87314.1"
/db_xref="GI:40539057"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="predicted by fgenesh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oryza sativa/mol_type="genomic_DNA"/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="OSJNBb0106M04.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="OSJNBb0106M04"
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                                                                                                                                                                                                                                                                                                                                                                                       _family="Oryza"
                                                                           _family="Oryza"
                     family="(TA)n"
                                                                                                     family="Oryza"
lement(4845. .4)
                                                                                                                                                                                                                                                                                                                                    family="Oryza"
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                                                                                                     .4898)
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larlagavaafidaaaasadaaalvasdlsdfyrsgsdelpssyvqlaklaaspeysa
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Lvaaiysasstpgetsspmkwynliatgkgckaismwysyfysyavgyfydktihint
YDQLFQGLTNASHDAKVKELLVSVCNGAVETMVKATHYWMSNANYKSYGSGSNGAGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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5722. .5742
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15827. .15850
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GI:18181938 (Arabidopsis thaliana)"
complement(join(<6297. .6941,7799. .>8029))
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complement(4848. .48
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complement(10905...
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NGEVEEEEERRRQRRKVSNRLSARRSRARKQQRLEELRGESARLRAENRELAARLHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="OSJNBb0106M04.3"
complement(10905. .1136)
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/gene="OSJNBb0106M04.3"
/note="contains Pfam prof:
actor)"
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complement(20302..21405)
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complement(join(6297...)
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            Direct Submission
Submitted (01-JAN-2004) The Institute for Genomic Research, Submitted (01-JAN-2004) The Institute for Genomic Research, Sedical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Oct 4, 2003 this sequence version replaced gi:23343713.
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1 (bases 1 to 133449)

Buell, C.R., Yuan, O., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,

Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S.,

Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S.,

Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V.,

Yang, O.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J.,

White, O., Salzberg, S.L. and Fraser, C.M.

Mhite, O., Salzberg, S.L. and Fraser, C.M.

Oryza, sativa chromosome 3 BAC OSJNBb0106M04 genomic sequence
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Submitted (16-JAN-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                   Submitted (28-SEP-2002) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA (bases 1 to 133449)
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Oryza sativa chromosome 3 BAC OSJNBb0106M04
                                                                                                   Buell, R.
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                                                                                                                                                                                                                                                                                                                  ical Center Dr, Rockville,
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correspondence to:rice@tigr.org
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Pred. No. 5.7e+02;
0; Mismatches 46; Indels 0;
                                                                                                                                      Institute for Genomic Research, e, MD 20850, USA
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http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/fgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
This BAC overlaps with rice BAC OSJNBa0079B15 (AC099043) and OSJNBa0072F13 (AC133450).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genecan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC clone OSJNBb0106M04 is from Oryza sativa chromosome 3 The orientation of the sequence is from SP6 to T7 end of the
                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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FEATURES repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region CDS mRNA gene repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region source repeat\_region complement (4846...4899)
/rpt\_family="Oryza"
complement (4848...4897) /rpt\_family="Oryza" /rpt\_ /rpt\_family="Oryza" complement(4843...4 , zgr KGPAPPTSTSRGRATSHSSAPPRSCWTLTASHPPPRSAAGFALTTPFRVGVGTNRTVF SEHHPHKALPITSAPSRTDAAASMDAPVGEN" /translation="MASQSRLTISGAHAFFPYLSFPEYSLIHRNLPAVSSPLPPVDGE ASRPPGHRLHCLRPRPLPSRIVPTEAMEGRSKRRHRLGKPPPDLQAGAVGGCADGRGN /gene="\ 337 9 /codon\_start=1 /product="hypothetical protein" /protein\_id="AAR87314.1" /db\_xref="GI:40539057" organism="Oryza sativa"
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(cultivar="Nipponbare" gene="OSJNBb0106M04.1" note="predicted by fgenesh" gene="OSJNBb0106M04.1" 'note="japonica cultivar-group" clone="OSJNBb0106M04" chromosome="3" db\_xref="taxon:39947" location/Qualifiers .133449 \_family="Oryza" \_family="Oryza" family="Oryza" lement(4845. .4898) family="Oryza" lement (4845. .4899) family="Oryza" \_family="Oryza" family="(TA)n" family="Oryza" .4904 OSJNBb0106M04.1" .4899) (japonica cultivar-group)"

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complement(20087. .. >21405)
/gene="OSJNBb0106M04.4"
complement(20302. .21405)
/gene="OSJNBb0106M04.4"
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/gene="OSJNBb0106M04.2"

complement (join (6297. .6941,7799. .8029))

/gene="OSJNBb0106M04.2"

/codon star--
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/db_xref="GI:40539061"
/tb_xref="GI:40539061"
/t
AMQYMTDKSMVIATICITLCLHVLNGTRLLVTA"
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                                                                                                                                        /translation="MDSRLVAFSHRRRRWILLAAGGAAAVFGAYKIYHHPAVAARRRR LARLAGAVAAFLDAAAASADAALVASDLSDFVRSGSDELPRSYTQLAKLAASPEVSA TVSAISEAITAGILRGVGSDSGPGSGGGVALSDRLVDRLFSESGERLAAIAGSFEVRH LVAAIYSASSTPGETSSPMKWVNLIANGKGQKAISNWVEVFVSTAVGVFVDKTTHINT YDQLFQGLTNASHDAKVKELLVSVCNGAVETWVKATHHVMSNANYKSVGSGSNGAGEG WVETVSSTLAVPSNRKFVLDVTGRVTFETVRSFLEFALWKMHAGAKKGGNTVMDSGLR
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complement(20087. .>21405)
/gene="OSJNBb0106M04.4"
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/rot family="(TA)n"
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SRGFGFVEFADEAATLRALADDEMPNHYFRGRKVDVKKAERRHDHKQTSPSIKNQNDS
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GI:18181938 (Arabidopsis thaliana)"
complement(join(<6297 ..6941,7799. .>8029))
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/gene="OSJNBb0106M04.3"
complement (10905. .11360)
/gene="OSJNBb0106M04.3"
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/gene="OSJNBb0106M04.3"
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DSHEAVCKILLNRFHNLNGRDVEVKIAVFKSFTYSEAKYYHMRMDMSLSFITYYDGMV
HVHFYTFYTFGCVTFLAHLTHSGYGYGGFIDYSCYAYGGFIGHQHDLVGSYYYAKDYS
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ISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 150743)

CE 1 (bases 1 to 150743)

RS Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,
Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S.,
Fadrosh, D.W., Tallon, L.J., Koo, H., Zimmann, V., Hsiao, J., Blunt, S.,
Vang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J.,
White, O., Salzberg, S.L. and Fraser, C.M.
Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence
LUpublished
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Submitted (31-JUL-2004) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Mar 31, 2004 this sequence version replaced gi:37693579. Address all correspondence to:rice@tigr.org
                                                                                                                                                   Submitted (31-MAR-2004) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA (bases 1 to 150743)
                                                                                                                                                                                                                                                                                   Submitted (16-OCT-2003) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA 4 (bases 1 to 150743)
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-SEP-2002) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 150743)
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Pred. No. 5.7e+02;
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1e 3 BAC OSJNBa0072F13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 133449;
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                                                                                                                                                                                                              Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence,
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clone OSJNBa0072F13 is from Oryza sativa chromosome orientation of the sequence is from SP6 to T7 end of

end of the

BAC

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://CCR-081.mit.edu/GENSCAN.html), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/cgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSJNBb0094003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC overlaps with rice BAC OSJNBb0106M04 (AC107207) and
                                                                                                                                                        /rpt_family="AT_rich"
9757. .9778
                                                                                                                                                                                                                                                                                                                                                                                                                               GARRERRRSGCRRRLALWRLLRPRAQRREAVPFRDQARNTAALPRPLDVDAGVEAVPE
LLRAHRRGPRRRRGERGYAGWWGPSTSSRPSGLRAAGVVEFLRRLSTKEVRVRSSLAA
LGGTGIRVVGGAPNYDLPALAHGGTAATAAWIQAYPWMLFRFVIVGNEVAGADTQLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative Glycosyl hydrolases family 17 protein"
/protein id="AAR85038.1"
/db xref="G1:50872438"
/translation="MASSSSHRWRKGFYPRKDGFSNNGNTTNHIFGVELDTIVSSKFL
DRNDNHVSIDINSLKSIAVHTTGYYDDKTGAFHDLSLISGKAMQGVWTGRRFTDGEAG
                                                                                                                                                                                                                                                                                                                                                                               THAPLLANLYPYFIYSYNPGGMDISFALFTASERAAAGGGGVRARGGRRSGVERRRAR
                                                                                                                                                                                                                                                                                                                                                                                                             PAMENVHAALAVAGLGHIKVTTSISQATIGIHIPPSASEFTDEAKSSFLSYVIPFLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="OSJNBa0072F13.1"
complement (join(3737. .4313,4877.
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                                note="predicted by fgenesh"
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                                                                    gene="OSJNBa0072F13.2"
                                                                                                                                                                                                                                      rpt_family="(CGG)n"
                                                                                                                                                                                                                                                                                            rpt_family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="OSJNBa0072F13.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="contains Pfam profile PF00332: Glycosyl hydrolases
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/gene="OSJNBa0072F13.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cultivar="Nipponbare"
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mol_type="genomic DNA"
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                                                                                                                       family="AT_rich"
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                                                                                                                                                           /translation="MSSSF98PSSSPIPSSLSLLLSLSPGLSLRWGAAAAVAAGGGGG
GGRERQRRRRRYMGELKRALDARCHMLLEMPTGTGKTAASSSPYKRHYDDTLDEDRST
PPRGRHKKLATCRTKQIGAIFMYANSEVLKCYTTGYTVPSAWDGIASSCTISLSHVFS
ACVTAADDSFMVAVIACSSLPPVTAPMRTLDDDVGMWTVEDAASATSSGMRHGWWRTR
                                                                                                                                                                                                                                                                                                                                                                                     24718. .24979))
/gene="OSJNBa0072F13.4"
                                                                                24815. .24883
                                                                                                           GITGDDLRRGSWRMPPPATSSGTIRGQWDHRRRRF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted by fgenesh"
complement(join(<21609. .221)
24718. .>24979))
/gene="OSJNBa007ZF13.4"
                                                                                                                                      PLTMSPAWGVAEEDAATGDELRRGTWMAEDVAAPATISGVDRGGCRCRRQALARDVDG
                                                                                                                                                                                                                                                                    /Codon_start=1
/product="hypothetical protein"
/protein_id="AAT85044.1"
/protef="GI:50872444"
/db_xref="GI:50872444"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (21609. .24979)
/gene="OSJNBa0072F13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YREELERPILEAAEFFSRVETÖLDSLAGTGSSEEEQDPSDKOLKHQLLRKYGGSLGDL
RQVFSKRTKKGKLPKEARQKLLHWWELHYKWPYPSEMEKMTLAQTTGLDQKQINNWFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MESFASLAGGGSSSTTARLPELISPENDHISPPPLLYQLLAGPESSARQHGHDGHHHGGGGGEAAAAAVQGQVSPAGAEAAVKAEIMSHPQYSALLAAYLG
CKKYGAPPDYLTKLTAVPAAQQLDEADGHPRARHEPQRDDDPDQLDQFMDAYCSMLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="nearly identical to knotted1 type homeobox protein OSH43 GB:BAA79225 1 GI:5103727 (Oryza sativa), Regional expression of the rice KN1 type homeobox gene family during embryo, shoot, and flower development (Plant Cell 11 (9), 1651 1664 (1999)); contains Pfam profile PF03790: KNOXI domain and PF03791: KNOX2 domain; EST cDNA AK107296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQRKRHWKPTPVAGTAFPTMEAAGGGFRHSGHGGGLAAAAALPLYMGRPFVVDGMYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(14329. .14836,14939. .15135,18892. .19000,
19127. .19264,19398. .19852))
/gene="OSJNBa0072F13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich"
complement(14329. .19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="knotted1-type homeobox protein"
protein_id="AAT85041.1"
db_xref="GI:50872441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9127. .19264,19398. .1
| gene="OSJNBa0072F13.3"
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}TSSLGGGrrrwGgTrggcerekeatvtamtaplsppleapvlatedheddvvvvvaa
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/protein_id="AAT85039.1
/db_xref="GI:50872439"
                                                                                                                                                                                                                                                                                                                                                                                                                         omplement (join (21609.
1718. .24979))
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0072. 10542
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_family="GA-rich"
                                                     family="(CCG)n"
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9.1"
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AUTHORS
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LOCUS
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1 (bases 1 to 150743)

Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S., Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hejao, J., Blunt, S., Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V., Yang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.
Oryza sativa chromosome 3 BAC OSUNBA0072F13 genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 CGTCGAGTCGGCGGCCGCCGACTGACGATGAGCGAGATGACCAGCTCCG 113
clone.

Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/),
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (31-JUL-2004) The Institute for Genomic Research, Submitted (21-JUL-2004) The Institute for Genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-MAR-2004) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA 5 (bases 1 to 150743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC133450 DNA linear PLN 31-JT Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence.
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                                                                                                                                                                    BAC clone OSJNBa0072F13 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-OCT-2003) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA 4 (bases 1 to 150743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (12-SEP-2002) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 150743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buell,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buell, R.
                                                                                                                                                                                                                                                                                                                    Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/note="nearly identical to P type R2R3 Myb protein
/note="nearly identical to P type R2R3 Myb protein
/note="nearly identical to P type R2R3 Myb protein
/note="nearly identical type R2R3 Myb protein
/note="nearly identical type R2R3 Myb genes
/note="nearly identical type R2R3 Myb protein
/note="nearly identical to P type R2R3 Myb protein
/note="nearly identical type R2R3 Myb protein
/note="near
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research,
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genscan and Genscan+ (Chris Burge, http://cCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://cCR-081.mit.edu/GENSCAN.html), GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/edby/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://stp.genome.washington.edu/RM/RepeatMasker.html).
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Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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                                                                                                                       SGWPQAGERAAG"
                                                                                                                                                                            llrahrrgprrrrgergyagwwgpstssrpsglraagyvbflrrlstkevrvrsslaa
lggtgirvvggapnydlpallahggtaataawiqaypwmlfrfvivgnevagadtqllv
pamenvhaalavaglghikvttsisqatigihippsaseftdeakssflsyvipplew
                                                                                                                                                                                                                                                                /translation="masssshrwrkgfyprkdgfsnngnttnhifgveldtivsskfl
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garrerrsgcrrrlalwrllrpragrreavpfrdgarntaalprpldvdagveavpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt family="(CCCG)n"
complement(3737. .8420)
/gene="OSJNBa0072F13.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="OSJNBa0072F13.1"
complement (join(3737. .4313,4877. .5250,7227.
8374. .8420))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (<3737. .4313,4877.
                                                                                                                                                    THAPLLANLYPYFIYSYNPGGMDISFALFTASERAAAGGGGVRARGGRRSGVERRRAR
                                                                                                                                                                                                                                                                                                                                                   /product="putative Glycosyl hydrolases family 17 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family 17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="R2443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="japonica cultivar-group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="OSJNBa0072F13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="OSJNBa0072F13.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="contains Pfam profile PF00332: Glycosyl hydrolases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .150743
                                                        _family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            __family="T-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSJNBb0106M04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5250,7227.
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/note="predicted by fgenesh"
<10072. .>10542

gene="OSJNBa0072F13.2"

family="AT\_rich"

rpt\_family="AT\_rich"

'gene="OSJNBa0072F13.2" .0072. .10542 'gene="OSJNBa0072F13.2"

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gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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                                                                                    repeat_region
                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="nearly identical to knotted1 type homeobox protein OSH43 GB:BAA79225 1 GI:5103727 (Oryza sativa), Regional expression of the rice KN1 type homeobox gene family during embryo, shoot, and flower development (Plant Cell 11 (9), 1651 1664 (1999)); contains Pfam profile PF03790: KNOX1 domain and PF03791: KNOX2 domain; EST cDNA AK107296 from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AT_rich"
complement(14329..19852)
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STSSLGGGRRRWGGTRGGCEREKEATVTAMTAPLSPPLEAPVLATEDHEDDVVVVVAA
VATSSALASSARWRERVEKAAAAVAAGEGDEGDGAGARGREREGKDGDGAERRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16530.
/rpt_f:
19984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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RQVFSKRTKKGKLPKEARQKLLHWWELHYKWYPYESENEKMTLAGTTGLDVATTEVULTUNTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join(14585. .14836,14939. 19127. .19264,19398. .19712))
/gene="OSUNBA0072F13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (
19127. .192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NORKRHWKPTPVAGTAFPTMEAAGGGFRHSGHGGGLAAAAAALPLYMGRPFVVDGMYRL
GS"
                                                                                                                                                                                 PPRGRHKKLATCRTKOIGAIFWYANSEVLKCYTTGYTVPSAWDGIASSCTISLSHVFS
ACVTAADDSFWVAVIACSSLPPVTAPWRTLDDDVGMWTVEDAASATSSGMRHGWWRTR
PLTMSPAWGVAEEDAATGDELRRGTWWAEDVAAPATISGVDRGGCRCRRQALARDVDG
                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(21609. .22157,23140. 24718. .24979))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAT85039.
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ggrerorrrrymgelkraldarchmllemptgtgktaassspykrhvddtldedrst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OSJNBa0072F13.3"
                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
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note="nearly identical to P type R2R3 Myb protein/
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                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="(CAG)n"
                                                                _family="GA-rich"
                                                                                                               family="(CCG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .11855
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                                                                                                                                          .24883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .22157,23140. .23202,24095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .15135,18892. .19000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .23202,24095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 41
AY081837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                   Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117132 GCTTCGGGTCGGACTCGCGGTTCGGCGGCGGCGGCGACGACCTCCGG 117083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 TGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B973 bp DNA linear BCT 20-APR-2(Bradyrhizobium japonicum isolate ppw200P9-2 putative amidase AmiC (amiC) gene, partial cds; pyruvate dehydrogenase (poxB), 2-dehydro-3-deoxyphosphogalactonate aldolase (dgoA), 2-dehydro-3-deoxygalactonate kinase (dgoK), putative alkanal 2-dehydro-3-deoxygalactonate kinase (dgoK), putative alkanal monooxygenase (luxA2), HpaC (hpaC), and sigma 54 activator (acoR) genes, complete cds; and unknown genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 CGGAGCTGGTCATCTCGTCGAGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradyrhizobium japonicum
Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-MAR-2002) Biology, Cell Biology and Applied Botany, Philipps University Marburg, Karl-von-Frisch-Str., Marburg 35032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThKPK2 insertions in the Bradyrhizobium japonicum poxB gene (pyruvate dehydrogenase) affect the symbiotic interaction within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY081837.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           soybean nodules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccecerricescracceesererricereccerecrecesecesecresareaseaseasea 117133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 8973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           origin of the typical two (Gene 326, 13 22 (2004)); Myb like DNA binding domain gene"
                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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/isolate="pPM200P9-2"
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origin of the typical two and three repeat Myb
(Gene 326, 13 22 (2004)); contains Pfam profile
Myb like DNA binding domain; EST cDNA AK112018 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       j̃oin(30040. .30277,30406. .30535,30701. .31699)
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GLGHHYDVALPELDPRAAFEAQTMCYISNEAVVISNMLAARGLDKPPEDLIEFMNIRI

WEAGRHTSPAERAKNGGVFNITSRGFGAFFEQMDVILTPITALPTPKVGTREYLTISD

NPDVLDWFGNLWRFFAFTELANLCGMPAISMPMATQDHDLPLGIQAIAKQANDGLLLQ
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note="ORF197; conserved hypothetical protein'
                                                                                                                                                                                                                                                                                                                           gene="amiC"
                                                                                                                                                                                                                                                                                                                                                                            'gene="amiC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:20257158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36.4;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         japonicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nree repeat Myb genes
ns Pfam profile PF00249:
cDNA AK112018 from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 150743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCT 20-APR-2002
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RLIGS FVHGSMANAMPQA I GAQASQPGRQV I SLSGDGGFTMLMGDL I TLTQMKL PVKV
VVFNNGVLGFVALEMKAAGFVDTNVDLQNPDFAAMARAMG I FAKRVEDPGELPGAVKE
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WIRAHPDPGGAGGSGWPVRPQPVRALPRHPRQRRTAR"
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                                                                                                                                                                                            complement (5383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="putative KHG/KDPG aldolase"
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CDS

gene

gene

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AY081837 B973 bp DNA linear BCT 20-APR-200 Bradyrhizobium japonicum isolate ppM200P9-2 putative amidase AmiC (amiC) gene, partial cds; pyruvate dehydrogenase (poxB), 2-dehydro-3-deoxyphosphogalactonate aldolase (dgoA), 2-dehydro-3-deoxygalactonate kinase (dgoK), putative alkanal monooxygenase (luxA2), HpaC (hpaC), and sigma 54 activator (acoR)
yenes, complete cds; and AY081837
                                                                                                                                                                                                                                                                                                                                                      GATCGCGACCAGCGGACGCTTCATCGACGGAAAGGGA 5359
                                                                                                                                                                                                                                                                                                                                                                                                         GATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGGCCTCGATCAGCACGCTGACGATGGACTCGGCCTCCTCCGGCTTGACGCCGCGCAG 5322
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6521. .7618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (8407. .8973)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPRRARALKLSRATLYRKIKHLKIETAQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.2; DB Pred. No. 1e+03;
                                    unknown
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                              genes.
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JOURNAL
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AUTHORS
TITLE
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TITLE
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Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Submitted (04-MAR-2002) Biology, Cell Biology and Applied Botany,
Submitted (04-MAR-2002) Siology, Cell Biology and Applied Botany,
Philippe University Marburg, Karl-von-Frisch-Str., Marburg 35032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller, P.

ThKPK2 insertions in the Bradyrhizobium japonicum poxB gene
(pyruvate dehydrogenase) affect the symbiotic interaction within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                       complement (2945.
                                                                     complement (2945. .4654)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="unknown"
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transl_table=
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"mol_type="genomic DNA"

'strain="USDA110spc4"

'isolate="pPM200P9-2"
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LTFSGQKGVNGDDRFAFGQWTRGATGAPVLTDAVAAFDCELAQEFETKTHSIFVGEVR
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7615. .8229
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FGYJAASGLPSDMAMENVGDMSGQNBOMTREALETILIKMTDDPAPWTYKKKFMYTYKBD
TMPDFLKPHIKPLQAPHPPNRVAGLSKNSDTLKLAGERGFIPMSLNLNPAYVGSHWDS
                                                                                                                                                                                                                                                                                                                                                                                                           HKAEAWHHSLSLLSSEVMPRLKHLGSAKKAA"
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KNYLKHAÞDVÞDRHVTVEYCAKRNWIVGSÞATVAEKIEKIYDEVGGFGVLLVFGFDYK
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/gene="luxA2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLLFGGTAAAARETLSGTLIGAELAAGLSGNVPKTGITLVASGRLATLYQLAFDELSV
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STFMTGELFSVISRDTILSLAVAGADDAEDVASFKAAVKAAFEAPAFAANLLFGARSR
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SDQNFAEYIKGGVTAFGLGSSLYKPGMSAADVAARAKQTIAAYDRAIVKD"
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WIHVRHEEVAAFAAAGEAQWTGSLAVCAGSCGFGNIHLINGLEDAHSSRVPVLAIAAQ
IPSABIIGGGYFQETHPQNLFRECSHYCELVSDASQLFPVISNAIRAVGLERCVAVIAN
PGDVAFRDPPRRALSTARGLALSAPKVVPEANELKALADLLNGAERITLFCGRGCAGA
HAPLANGLAEALKSPIVHALGGKEHVEYENPYDVGWTGFIGFSGSYAAMHACDALVMLF
TÜBPYKOFFFTGCQIAQIDIR PENLEGRRQADHFRGRSAAABDQDPAQAYSTMYSRITRR
RARGWTRSPGAPPGSKPIHPQYLAKVVSDHASEDAVFTADVGTFTVWAARYLEMNGRR
RALIGSFVHGSNALMWPQAIGAQASQPGRDVISLSGDGGFTMLMGDIITLTQWKLPVKV
VVFNNGVLGFVALEWKAGFVDTNVDLQNDFJSAMARAWGIFAKKVEDPGSLPGAVKE
LJGHNGRALLDVVTAKQELSMPPTITTEQIKGFSLWVLRAVNNGRGGRGARCLAKTNL
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protein_id="AAM12353.1"
db_xref="G1:20257168"
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                                                                                                                                                                                                                                                                                                                                    Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 28, 2001 this sequence version replaced gi:7709299.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Submitted (03-AUG-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459

Obsect to 123169)

DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                 STS Content:
SHGC-84992 G53847
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 123169)
DOB Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                     Quality: Phrap Quality >=40 99.3% of Sequence; Estimated Total Number of Errors is 0.9.
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DOE Joint Genome Institute.
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nmrQlrhvlrlagctaengvvtdadldlplfggraadgprggrarddrrgaaQawrsc
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complement(8407. .8973)
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/db_xref="taxon:9606"
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                                                                           /organism="Homo sapiens"
/mol type="genomic DNA"
                                                                                                                                      Location/Qualifiers
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Best Local Similarity 55.0
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On Feb 28, 2001 this sequence version replaced gi:7709299.
Draft Sequence Produced by DOE Joint Genome Institute
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Finishing Completed at Stanford Human Genome Center
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Submitted (03-M05-1999) Production Sequencing Facility, DOB Submitted, 2800 Mitchell Drive, Walnut Creek, CA 9455
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9455
1 (bases 1 to 123169)
DOB Joint Genome Institute and Stanford Human Genome Center.
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/db_xref="taxon:9606"
/chromosome="5"
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Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (01-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTD-2327L5, complete sequence.
AC018764
AC018764.8 GI:28933541
                                                                                                                                                                                                                                                                                                                                                                    Quality: Phrap Quality >=40 99.6% of Sequence; Estimated Total Number of Errors is 0.6. Retriated Total Number of Errors is 0.8. NOTE: Bacterial transposon excised at 89327. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute and Stanford Human Genome Center.
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US-09-902-540-8058
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US-09-902-540-821
US-09-902-540-821
US-09-902-540-3318
US-09-902-540-3318
US-09-902-540-53311
Sequence 15737, A
Sequence 8973, Ap
Sequence 8973, Ap
Sequence 8973, Ap
Sequence 3748, Ap
Sequence 7905, Ap
Sequence 7905, Appli
Sequence 13826, A
Sequence 1182, Ap
Sequence 1182, Ap
Sequence 13526, A
Sequence 13933, A
Sequence 13933, A
Sequence 13933, A
Sequence 13933, A
Sequence 13826, A
Sequence 1467, Appli
Sequence 3619, Ap
Sequence 3619, Ap
Sequence 3619, Ap
Sequence 1116, Appli
Sequence 1116, Appli
Sequence 1117, Ap
Sequence 1116, Ap
Sequence 1117, Ap
Sequence 1112, Appl
Sequence 211, Appl
Sequence 211, Appl
Sequence 21112, Ap
Sequence 3031, Ap
Sequence 3311, Ap
Sequence 3311, Ap
Sequence 3311, Ap
Sequence 3311, Ap
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RESULT 1 US-09-434-288-7

ALIGNMENTS

Sequence 7, Applicati Patent No. 6303767 GENERAL INFORMATION:

7, Application US/09434288 o. 6303767

APPLICANT:

Betlach C., Melanie McDaniel, Robert

McDaniel,

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TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA TITLE OF INVENTION: CONSTRUCTS THEREFOR FILE REFERENCE: 30062-20030.00
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-103-840A-2
                                                                        Matches
                                                                                                            Query Match
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Best Local Similarity 59.2
58; Conservative
                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                     ORGANIAM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                      TYPE: DNA
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TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                         ENGTH: 4403765
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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                                                                                     Local Similarity
37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGGGGCGGCCGACTCGACGATGAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 CCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
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                                                                    Conservative
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                                                            Score 34; DB 3; Length 4403765;
Pred. No. 10;
0; Mismatches 40; Indels 0;
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Pred. No.
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RESULT 2 US-09-434-288-7/c

Sequence

GENERAL INFORMATION:

Sequence 7, Application US/09434288 Patent No. 6303767

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424

; TYPE: DNA ; ORGANISM: Streptomyces narbonensis US-09-434-288-7

SOFTWARE: 1

PatentIn Ver. 2.1

LENGTH:

1681

FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12

Query Match Best Local Similarity Matches 66;

Conservative

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52; ω --

22.6%;

Score 34.8; DE Pred. No. 4.6; 0; Mismatches

DB

Length 1681; Indels

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SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptomyces narbonensis
                                                                                                                                                                                                                                                                   JENGTH: 1681
                                                                              541
                                                                                                37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTGACGATGAG 96
CGACCGGAGCGCCGCCGCCGCGACCCGCGGGTGAGCCGCTGAGCAGCGGCGCCAG 424
                         CGAGATGACCAGCTCCGGCCGCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                 PatentIn Ver. 2.1
                                                                                                                                             Conservative
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                                                                                                                                                            22.6%;
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4251891 GCGGTTGAAGATGATCACCACGCCCACCGACTGGCCGCGATACGGCGGCTACGCGCTGGC 4251832

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APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2
SEQ ID NO 1
LENGTH OF SEQ ID NOS: 2
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US-09-103-840A-1/c
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Best Local
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                             LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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4259635 GCGGTTGAAGATGATCACCACGCCCACCGACTGGCCGCGATACGGCGGCTACGCGCTGGC 4259576
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                                37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGACTCGACGATGAG
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                                                                       Conservative
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                                                                     Score 34; DB Pred. No. 10; O; Mismatches
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                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4417
LENGTH: 747
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SEQ ID NO 4417
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1999
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                       61;
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TGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACCGATGAGCGAGAT 139
                                                     ACTGCTCGATGCGCGCCAGAGCCTGCGTCGGCCGCTGAC
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                                                                                    Application US/09252991A
                                                                                                                       Conservative
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                                                                                                                                      21.7%;
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Pred. No. 9.8;
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Pred. No. 9.8;
                                                                                                                       Mismatches
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GCTGCGCCACCGCCGTCGCCGGCCTCCTGCCAGATGTCCATCAT 412

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PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33147
LENGTH: ---
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                                                                                                                                                                                                                                            ; TYPE: DNA
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4622
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US-09-252-991A-4622
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                                                                                                                                                                                  Matches
                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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SEQ ID NO 4622
LENGTH: 3225
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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                                                                                                                 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 CATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                        GCTGCGCCACGGCCTCGCCGGCCTGCTGCCAGATGTCCATCAT 8
                                                                       TGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGAT 139
                                                                                                       ACTGCTCGATGCGCCCAGAGCCTGCGTCGGCCGCTGAC 114
                                                                                                                                                                               Conservative
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UMBER: US 60/074,788
1998-02-18
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Pred. No. 11;
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Pred. No. 11;
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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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US-09-513-999C-8640/c
; Sequence 8640, Application US/09513999C
; Patent No. 6783961
                                                                                                                                                                             RESULT 12
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-513-999C-8640
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US-09-513-999C-8640
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SEQ ID NO 8640
LENGTH: 345
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: m=a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: y=c
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LOCATION: 73
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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LOCATION: 319
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                                                                                                                                                                                                                              306 CCACCCAGCCTACYKYC 322
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SOFTWARE: Patent.pm SEQ ID NO 8640

LENGTH: 345 TYPE: DNA ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc\_feature
LOCATION: 73
OTHER\_INFORMATION: n=a,

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NAME/KEY: misc\_feature LOCATION: 319
OTHER INFORMATION: y=c

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NAME/KEY: misc\_feature LOCATION: 320

OTHER INFORMATION: k=g

or t

FEATURE:

OTHER INFORMATION: y=c NAME/KEY: misc\_feature LOCATION: 321

or t

OCATION: 336

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FEATURE:
NAME/KEY: misc\_feature
LOCATION: 345 OTHER INFORMATION: k=g NAME/KEY: misc\_feature PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681

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                                                                                                                APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2360
LENGTH: 1110
TWODE: NAM
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Patent No. 6033....
Patent No. 6033....
Patent No. 6033....
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                                     Query Match
                                                                          ORGANISM: Myxococcus xanthus
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.09-513-999C-8640
                                                                                                              TYPE: DNA
 Local Similarity 60.0
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Similarity 62.3%;
48; Conservative
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                 21.0%;
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Score 32.4; DB 4; Length 1110; Pred. No. 18; 0; Mismatches 36; Indels 0
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SEQ ID NO 2360
LENGTH: 1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Appli
Patent No. 541003
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ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,651
PILING DATE: 1920224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      APPLICANT: Pajor, Ana rate Applicant: Wright, Ernest M
APPLICANT: Wright, Ernest M
TITLE OF INVENTION: Cloning and Functional Expression of a
TITLE OF INVENTION: Mammalian Na+/Nucleoside Cotransporter: A Member of the
TITLE OF INVENTION: SGLT Family
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
ADDRESSEE: Sheldon & Mak
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                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848
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Pred. No. 1
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                                                                                                                                   Version #1.25
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REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:

8772

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RESULT 16
US-07-841-651-1/c
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Matches
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                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/841,651
FILING DATE: 19920224
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                                          TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Mandel, SaraLynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 8772
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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HYPOTHETICAL: NO
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ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake A
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pajor, Ana M
APPLICANT: Wright, Ernest M
TITLE OF INVENTION: Cloning and
TITLE OF INVENTION: Mammalian Na
TITLE OF INVENTION: SGLT Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
           TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                       CITY: Pasadena
STATE: California
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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LOCATION:
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                         2238 base pairs
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(818) 795-6771
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double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.0%;
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                                                                                                                      8772
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Pred. No. 18;
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RESULT 18
US-09-902-540-1100/c
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; ORGANISM: Myxococcus xanthus
US-09-902-540-1100
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APPLICANT: Goldman, Barry J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiggand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR TILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1100
LENGTH: 15447
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                       Sequence 1100, Application US/09902540 Patent No. 6833447
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)8
CCURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Pred. No. 20;
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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; ORGANISM: Myxococcus xanthus
US-09-902-540-1100
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8862
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US-09-252-991A-8862
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                                                                                                                                                                                                                                                                                                             RESULT 20
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NUMBER OF SEQ ID NOS: 16925
SEQ ID NO 1100
LENGTH: 15447
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PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 8862
                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                  Sequence 8862, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                     APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                  PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                              APPLICANT:
NUMBER OF SEQ ID NOS:
EQ ID NO 8862
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1998-07-27
                                                                                                                                                                           Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                       AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                          1998-02-18
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Pred. No. 20;
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Pred. No. 19
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APPLICANT: MAIC J. Rubenfield et al.
ITILE OF INVENTION: NUCLEIC ACID ANINO ACID SEQUENCES REL
ITILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTI
ITILE REFERENCE: 107196.136
CURRENT PILICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15671
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                                                                                                                                                                                                                                                                                                                         Sequence 15671, Application US/09252991A Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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TYPE: DNA
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ORGANISM: Pseudomonas aeruginosa
                     TYPE: DNA
                                   ENGTH: 807
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Pred. No. 20;
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Pred. No. 1
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RESULT 24
US-09-252-991A-8753/c
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8753
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US-09-252-991A-8753
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                                                                                                                         PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8753
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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NUMBER OF SEQ ID NOS:
SEQ ID NO 8753
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  Query Match
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                          FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                          LENGTH:
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  20.9%;
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  Score 32.2;
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Pred. No. 20;
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GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO FITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FITTLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15578

LENGTH: 1203
                                                                                                                                       FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15578
LENGTH: 1203
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US-09-252-991A-15578/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15578, Application US/09252991A Patent No. 6551795
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                   Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                          TYPE: DNA
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                                                                                                       ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              676 CAGCCCGAGCTGCTCGCGGAAATCGGCGTCGCGTACCGCAGCGCAGTTGGCCGCGTAGCC 735
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15737
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15737
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US-09-252-991A-15737
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SEQ ID NO 15737
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SEQ ID NO 15737
LENGTH: 1869
                                                                                                                                                           Matches
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Patent No. 6551795
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1869
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1252 CAGCCCGAGCTGCTCGCGGAAATCGGCGTCGCGTACCGCAGCGCAGTTGGCCGCGTAGCC 119:
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Pred. No. 20;
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Pred. No. 20;
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                                                                                                                                                                                                                       Length 1869;
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                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 8973
LENGTH: 1899
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GENERAL INFORMATION:
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SEQ ID NO 8973
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                                                                                                                                                 Matches
                                                                                                                                                                                     Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                1879 GGCATGATCTGCCCGTTGCCCTCGGCGGCGTTGCGGCCGATGGTTGATGGTCGCCTCGGCG 1820
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62 ATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
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                                                                                                                                                                    Similarity
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6551795
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                                                                                                    egcegagergarearercecrearegergagerggegeegeegeagerggrearercecre 61
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                                                                                                                                               Conservative
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Pred. No. 20;
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1819

ATCGGCTTGCCGGCGCAGCAATACTCGTTGAGGGTCGGGGT 1779

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US-09-902-540-3748/c
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PRIOR ETLING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 3748
LENGTH: 921
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                      Matches
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                                                                                                                                                                                         Query Match
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
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Best Local Similarity 62.5%;
Matches 50; Conservative
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LENGTH: 921
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                                                                                                                                                                                                                               .09-902-540-3748
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)8
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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                                                                                                      28 GTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGGCCGACTC
                                                                                                                                                    l Similarity
50; Conserv
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GGCGCCGGTGGAGATGCCCA 782
                                                                   GGCGAGCACGCGGCTGCCGTCGTCATCTCGCCCAGCTTCTGATTCACGGCGGACAGCGC 802
                                 GACGATGAGCGAGATGACCA 107
                                                                                                                                                    Conservative
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                                                                                                                                                                    20.8%;
                                                                                                                                                0; Mismatches
                                                                                                                                                                    Score 32; DB
Pred. No. 22;
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Pred. No.
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Sequence 7905, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

ITITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Use

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

ETICRAPTICATION TOMBER: US/09/902,540

PRIOR APPLICATION NUMBER: GO/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 7905

LENGTH: 1093
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APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 500-07-10

PRIOR APPLICATION NUMBER: 500-07-10

SPRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 500-07-10

PRIOR APPLICATION NUMBER: 500-07-10

PRIOR APPLICATION NUMBER: 500-07-10

PRIOR DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

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US-09-902-540-7905
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 68; Conserv
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Best Local Similarity 53.1%;
Matches 68; Conservative
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                                                                                                                                                      408
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                                                                                 61
                                                                                                                                                                                                                                                                                                 68;
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                                                         CATCGTCGAGTCGGCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGG 120
                                                                                                                                   ccecercaecrecicceacaececererecaeeceaeereaeececececrececricece 349
                                                                                                                                                                                                                ceecceeaecreercarcicercarcercaecreeceeceeceercarcicec 60
CTCCGCCGACGACGCCTGCGCCAGCCCGGTGAGCTGACCGCTCAGCTCCTGCGAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCGGAGGGCGAAGCGGAGCGCCCACCTCGCCCTGCACACGGCGCTGTCGGACGAGC
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                                                                                                                                                                                                                                                                                                                                20.8%;
                                                                                                                                                                                                                                                                                         Score 32; DB of Pred. No. 22; 0; Mismatches
                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                               4; Length 1093;
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RESULT 35
US-09-032-372-6
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US-09-032-372-6
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                                                                                                                                                                                         Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 31.
CITY: Palo Alto
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                           MEDIAL
LIBRARY: Since 78191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herew. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
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 271
                                                          211 CACGAGAACGAGACGCTGGCGTCGCTGAAGAGCGAGGCCGAGAGCCTCAAGGGCAAGCTG
                                                                                                                  151 CGAGGETETECETTECETETECGETGEGTECECGEGEGAAGATGGEAACCGAGGGGETG
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                                                                                                                                                                             74;
                           GACGATGAGCGAGATGACCAGCTC 148
                                                                                     CGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCTCATC 64
GAGGAGGAGCGAGCCAAGCTGCAC 294
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                   SYNORAB01
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Corley, Neil C.
Guegler, Karl J.
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Pred. No. 23;
0; Mismatches
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                                                                                      124
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RESULT 37
US-09-902-540-797
; Sequence 797, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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US-09-032-372-6/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
PRATESEO FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/032,372 FILING DATE: Herewith
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ADDRESSEE: Incyte Ph
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
TITLE OF INVENTION: CEI
NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: Sime 78191
                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                174
                                                                                                                                           127
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                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                74;
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                                                                                                                CGGAGAGGGAAGCGGAGAGCCTCG
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3174 Porter Drive
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Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                              DB 3;
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; ORGANISM: Myxococcus xanthus
US-09-902-540-797
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US-09-902-540-797/c
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                                                                                                                                                                                                                                                                                                                         SEQ ID NO 797
LENGTH: 7994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 797
LENGTH: 7994
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goldman, I
APPLICANT: Hinkle, (
APPLICANT: Slater, (
APPLICANT: Wiegand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Myxococcus xanthus
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APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15849) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICANT: Goldman, Barry S.
PLICANT: Hinkle, Gregory J.
PLICANT: Slater, Steven C.
PLICANT: Miegand, Roger C.
PLICANT: Miegand, Roger C.
PLICANT: Miegand, Roger C.
PLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
PLE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                   Match 20.8%;
Local Similarity 53.1%;
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                                 ACTCGACG 128
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                                                              CTCCGCCGCGACGACGGCCTGCGCCAGCCCGGTGAGCTGACCGCTCAGCTCCTGCGAACG
                                                                                              CATCGTCGAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG
                                                                                                                              CCGCGTCAGCTCGTCCGACAGCGCCGTGTGCAGGGCGAGGTGGGCGCGCTCCGCTTCGCC
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Pred. No. 25;
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Pred. No.
                                                                                                                                                                                                 Mismatches
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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: unsure
; LOCATION: (1)..(17897)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1182
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1182
LENGTH: 17897
                                                                                    Matches
                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1182, Applic Patent No. 6833447 GENERAL INFORMATION:
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LENGTH: 17897
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome
FILE REFERENCE: 38-10(15849)B
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10
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GENERAL INFORMATION:
                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
NAME/KEY: unsure
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                            ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                       TYPE: DNA
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13468 GGCGAGCACGCGGCTGCCGTCGTCATCTCGCCCAGCTTCTGATTCACGGCGGACAGCGC 13409
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                             28 GTCGAGTCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTC
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Pred. No. 25;
0; Mismatches
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Pred. No. 25;
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US-09-252-991A-13526/c
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US-09-252-991A-13526
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LENGTH: 2496
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SEQ ID NO 13526
LENGTH: 2496
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Best Local (
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Patent No. 6551795
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-09-252-991A-13526
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Local Similarity 62.8%;
les 49; Conservative
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GGCCATCTGCGGCTGCAG 1013
                                                                       GACCAGCTCCGGCCGCCG 120
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ilarity 62.8%;
Conservative
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JMBER: US 60/094,190
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Pred. No. 29;
0; Mismatches
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Pred. No. 29;
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LENGTH: 2622
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APPLICANT: Marc J.
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SEQ ID NO 13933
LENGTH: 2622
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                     Local
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49; Conserv
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CTGATCAGGATCTGTTCC 1569
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                                     AGCGAGATGACCAGCTCC 112
                                                                                                                                                   Conservative
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                   Score 31.6;
Pred. No. 29;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
FITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCUSIC ACID AND THERAPEUTICS
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FILLE REFERENCE: 107196.136
CURRENT FILING OATE: 1999-02-18
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PRIOR FILING DATE: 1998-07-18
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NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13826
LENGTH: 2685
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13826
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; Sequence 13826, Application US/09252991A
; Patent No. 6551795
Search completed: April 9, 2005, 00:55:08 Job time : 154 secs
                                                                                                                                                                                                                                                                                                           Query Match 20.5%; Score 31.6; DB 4; Length 2685; Best Local Similarity 62.8%; Pred. No. 29; Matches 49; Conservative 0; Mismatches 29; Indels 0,
                                                                                                  1636 GGCCATCTGCGGCTGCAG 1653
                                                                                                                                                                                                    1576 GGÁACAGATCCTGATCAGCACCGTCGGCGGCGCCGGCCGACGTCAAGCCGAAGAGCGAGAA 1635
                                                                                                                                                    103 GACCAGCTCCGGCCGCCG 120
                                                                                                                                                                                                                                        43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCCGACTCGACGATGAGCGAGAT 102
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